

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F:533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:535-671/Domain: flavodoxin homology <FLX>
 F:194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

52.6%; Score 41; DB 1; Length 1147;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAGCGPALYEDPPD 14

Db 305 ADGQDPEVFEIIPD 318

RESULT 15

S47647

nitric-oxide synthase (EC 1.14.13.39) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 16-Jun-2000

C:Accession: S47647; JCI472

R:Geng, Y.; Almqvist, M.; Hansson, G.K.

Biochim. Biophys. Acta 1218, 421-424, 1994

A>Title: cDNA cloning and expression of inducible nitric oxide synthase from rat vascula

A:Reference number: S47647; MUID:94325351; PMID:7519448

A:Accession: S47647

A:Molecule type: mRNA

A:Residues: 1-1147 <GEN>

A:Cross-references: EMBL:X76881; NID:9439283; PIDN:CA54208.1; PID:9439284

R:Numokawa, Y.; Ishida, N.; Tanaka, S.

Biochem. Biophys. Res. Commun. 191, 89-94, 1993

A>Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells.

A:Reference number: JCI472; MUID:93191721; PMID:7680561

A:Accession: JCI472

A:Molecule type: DNA

A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10

A:Cross-references: DDBJ:D14051; NID:9286260; PIDN:BA03138.1; PID:9286261

A:Experimental source: vascular smooth muscle

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct

C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal

F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F:538-674/Domain: flavodoxin homology <FLX>

F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

52.6%; Score 41; DB 1; Length 1147;

Best Local Similarity 50.0%; Pred. No. 1.1e+02;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 AAGCGPALYEDPPD 14

Db 308 AHGQDPEVFEIIPD 321

Search completed: January 30, 2003, 14:38:54
 Job time : 18 secs

QY 3 GEGPALYEDPP 13
 1:||||:||||
 Db 579 GGGPAMTEDSP 589

RESULT 11

F88640
 Protein F52C12.4 [imported] - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
 C:Accession: F88640
 R:Anonymous, The C. elegans Sequencing Consortium.
 Science 282, 2012-2018, 1998
 A:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: F88640
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1453 <STO>
 A:Cross-references: GB:chr_IV; PIDN:MAC68958.1; PID:g3800950; GSPDB:GN00022; CESP:F52C12
 C:Genetics:
 A:Gene: F52C12.4
 A:Map position: 4

Query Match 53.8%; Score 42; DB 2; Length 1453;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LYEDPPD 14
 |||||
 Db 517 LYEDPPD 523

RESULT 12

A84567
 hypothetical protein At2g18660 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: A84567
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beutlo, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
 Neuss, D.; Niernman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84567
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-126 <STO>
 A:Cross-references: GB:AE002093; NID:g4185132; PIDN:AAD08935.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g18660
 A:Map position: 2

Query Match 52.6%; Score 41; DB 2; Length 126;
 Best Local Similarity 58.3%; Pred. No. 9.5;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGGPALYEDPP 13
 |:|:|:|:|
 Db 22 AAGKAYIDPP 33

RESULT 13

AT0617
 probable DNA methylase STY1014 [imported] - *Salmonella enterica* subsp. *enterica* serovar
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002
 C:Accession: AF0617
 R:Parhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AF0617

A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-293 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05408.1; PID:g16502169; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1014

C:Superfamily: mbra protein

Query Match 52.6%; Score 41; DB 2; Length 293;
 Best Local Similarity 58.3%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGGPALYEDPP 13
 ||:|:|:|
 Db 193 AGGDVYICDP 204

RESULT 14

A43271
 nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
 C:Species: *Mus musculus* (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000
 C:Accession: A43271; A42166; JN0458; A46186
 R:Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderik, K.M.; Lee, T.D.; Ding, A
 Science 256, 225-228, 1992
 A:Title: Cloning and characterization of inducible nitric oxide synthase from mouse m
 A:Reference number: A43271; MUID:92229444; PMID:1373522
 A:Accession: A43271
 A:Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-1144 <XIE>
 A:Cross-references: GB:M07039; NID:g198406; PIDN:AAA39315.1; PID:g198407
 R:Lyons, C.R.; Orloff, G.O.; Cunningham, J.M.

J. Biol. Chem. 267, 6370-6374, 1992
 A:Title: Molecular cloning and functional expression of an inducible nitric oxide syn

A:Reference number: A42166; MUID:92210618; PMID:1372907
 A:Accession: A42166
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-1144 <LYO>

A:Cross-references: GB:M84373; NID:g200095; PIDN:AAA39834.1; PID:g200096
 R:Wood, E.R.; Berger, Jr., H.; Sherman, P.A.; Lapetina, E.G.
 Biochem. Biophys. Res. Commun. 191, 767-774, 1993

A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric o
 A:Reference number: JN0457; MUID:93221515; PMID:7682072
 A:Accession: JN0458
 A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
 A:Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>

A:Experimental source: liver
 R:Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
 Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992

A:Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the bra
 A:Reference number: A46186; MUID:92357701; PMID:1379716
 A:Accession: A46186
 A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA
 A:Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>
 A:Cross-references: GB:M92649; NID:g200109

A:Experimental source: RAW 264.7 cells, macrophage
 A:Note: sequence extracted from NCBI backbone (NCBIP:113541)
 C:Genetics:
 A:Gene: NOS

C:Function: NOS
 A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein red

RESULT 8

T42699

Hypothetical protein DKFp434L0850.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C:Accession: T42699; T34559

R:Positix, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, November 1999

A:Reference number: Z22232

A:Accession: T42699

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-303 <AA>

A:Cross-references: EMBL:AL133042

A:Experimental source: adult testis; clone DKFp434L0850

R:Positix, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, October 1999

A:Reference number: Z21540

A:Accession: T34559

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-303 <POU>

A:Cross-references: EMBL:AL122038

A:Experimental source: adult testis; clone DKFp434L0850

C:Genetics:

A:Note: DKFp434L0850.1

Query Match

Best Local Similarity 53.8%; Score 42; DB 2; Length 303;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGECPALYEDP 12

DB 84 SAGEGPVIVHP 95

RESULT 9

A49676

Nitrlic-oxide synthase (EC 1.14.13.39), inducible - human

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 20-Jun-2000

C:Accession: A49676; JX0345; G01947; J38933; S47566; A47475

R:Charles, I.G.; Palmer, R.M.; Hickery, M.S.; Bayliss, M.T.; Chubb, A.P.; Hall, V.S.; Mc

A:Title: Cloning, characterization, and expression of a cDNA encoding an inducible nitric

A:Reference number: A49676; MUID:94068614; PMID:7504305

A:Accession: A49676

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1153 <RES>

A:Cross-references: EMBL:X73029; NID:9441452; PIDN:CAA51512.1; PID:9441453

R:Hokari, A.; Zeniya, M.; Esuami, H.

J. Biochem. 116, 575-581, 1994

A:Title: Cloning and functional expression of human inducible nitric oxide synthase (NOS)

A:Reference number: JX0345; MUID:95155267; PMID:7531687

A:Accession: JX0345

A:Molecule type: mRNA

A:Residues: 1-607, 'L', 609-1153 <HOK>

A:Cross-references: DDBJ:D26525; NID:9559326; PIDN:BA05531.1; PID:g1228940

A:Experimental source: glioblastoma cell line A-172

R:Park, C.; Park, R.; Krishna, G.

submitted to the EMBL Data Library, July 1995

A:Reference number: G08912

A:Accession: G01947

A:Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-607, 'L', 609-1153 <PAR>

A:Cross-references: EMBL:U31511; NID:9551320; PIDN:AAB49041.1; PID:g9551321

R:Guo, F.H.; De Raeye, H.R.; Rice, T.W.; Stuehr, D.T.; Thummler, F.B.; Erratum, S.C.

Proc. Natl. Acad. Sci. U.S.A. 92, 7809-7813, 1995

A:Title: Continuous nitric oxide synthesis by inducible nitric oxide synthase in normal

A:Reference number: I38933; MUID:95372368; PMID:7544004

A:Accession: I38933

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-675, 'I', 677-932, 'G', 934-965, 'A', 967-1153 <RES>

A:Cross-references: EMBL:U20141; NID:9687680; PIDN:AAB60366.1; PID:9687681

R:Maier, R.; Bilbe, G.; Rediske, J.; Lotz, M.

Biochim. Biophys. Acta 1208, 145-150, 1994

A:Title: Inducible nitric oxide synthase from human articular chondrocytes: cDNA clone

A:Reference number: S47566; MUID:94368816; PMID:7522054

A:Accession: S47566

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-22, 'G', 24-153, 'L', 155-176, 'V', 178-799, 'A', 801-912, 'P', 914-1153 <MAI>

A:Cross-references: EMBL:U05610; NID:94552487; PIDN:AA56666.1; PID:94552488

R:Geller, D.A.; Lowenstein, C.U.; Shapiro, R.A.; Nussler, A.K.; Di Silvio, M.; Wang,

Proc. Natl. Acad. Sci. U.S.A. 90, 3491-3495, 1993

A:Title: Molecular cloning and expression of inducible nitric oxide synthase from hum

A:Reference number: A47475; MUID:93234523; PMID:7682706

A:Accession: A47475

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-422, 'I', 424-804, 'D', 806-830, 'SP', 833-932, 'G', 934-965, 'A', 967-986, 'V', 98

A:Cross-references: GB:L09210; NID:9292241; PIDN:AA59171.1; PID:9292242

A:Experimental source: hepatocytes

C:Genetics: sequence extracted from NCBI backbone (NCBIP:129733)

A:Gene: GDB:NOS2A; NOS2, INOS

A:Cross-references: GDB:139215; OMIM:163730

A:Map position: 17cen-17q11.2

C:Function:

A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NAD

C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein red

C:Keywords: calmodulin binding; chromoprotein; FAD; Flavoprotein; FMN; heme; iron; me

F:509-529/Region: calmodulin binding #status predicted

F:539-1127/Domain: NADPH-ferrihemoprotein reductase homology <FLX>

F:541-677/Domain: flavodoxin homology <FLX>

F:623-654/Region: FMN binding #status predicted

F:765-778/Region: FAD-pyrophosphate binding #status predicted

F:903-913/Region: FAD-isoloxazine binding #status predicted

F:978-996/Region: NAD-ribose binding #status predicted

F:1076-1091/Region: NADP-adenine binding #status predicted

F:200/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match

Best Local Similarity 53.8%; Score 42; DB 2; Length 1153;

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAGECPALYEDPPD 14

DB 311 ANGRDPELFEIRPD 324

RESULT 10

I48378

hairless protein - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I48378

R:Cachon-Gonzalez, M.B.; Fennel, S.; Coffin, J.M.; Moran, C.; Best, S.; Stoye, J.P.

Proc. Natl. Acad. Sci. U.S.A. 91, 7717-7721, 1994

A:Title: Structure and expression of the hairless gene of mice.

A:Reference number: I48378; MUID:94329587; PMID:8052649

A:Accession: I48378

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-1182 <RES>

A:Cross-references: EMBL:Z32675; NID:9531706; PIDN:CAA83587.1; PID:g531707

Query Match 53.8%; Score 42; DB 2; Length 1182;

Best Local Similarity 63.6%; Pred. No. 80;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

C:Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus
F:2-317/Product: DNA repair enzyme APEX nuclease #status experimental <MAT>

Query Match

Best Local Similarity 94.9%; Score 74; DB 2; Length 317;
Pred. No. 5.9e-05;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGEGPAHYEDPPD 14
||||| |||||||

DB 36 AAGEGPAHYEDPPD 49

RESULT 4

S26830
DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - bovine

N:Alternate names: apurinic/apyrimidinic endonuclease I; BAP-1 protein
C:Species: Bos primigenius taurus (cattle)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Feb-2000
C:Accession: S26830; S30761

R:Robson, C.N.; Milne, A.M.; Pappin, D.J.C.; Hickson, I.D.
Nucleic Acids Res. 19, 1087-1092, 1991

A:Title: Isolation of cDNA clones encoding an enzyme from bovine cells that repairs oxid
A:Reference number: S26830; MUID:91212189; PMID:1708495

A:Accession type: mRNA
A:Molecule type: mRNA

A:Residues: 1318 <ROB>
A:Cross-references: EMBL:X56685; NID:g117; PIDN:CAA40014.1; PID:g118

A>Note: part of this sequence, including the amino end of the mature protein, was confir
R:Henner, W.D.; Kiker, N.P.; Jorgensen, T.J.; Munck, J.N.
Nucleic Acids Res. 15, 5529-5544, 1987

A:Title: Purification and amino-terminal amino acid sequence of an apurinic/apyrimidinic
A:Reference number: S30761; MUID:87289027; PMID:2441359

A:Accession: S30761
A:Molecule type: protein

A:Residues: 2-20, 'LP', 23 <HEN>
A:Molecule type: protein

C:Superfamily: exodeoxyribonuclease III
C:Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus

F:2-318/Product: DNA-(apurinic or apyrimidinic site) lyase #status predicted <MAT>

Query Match

Best Local Similarity 79.5%; Score 62; DB 2; Length 318;
Pred. No. 0.0067;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGEGPAHYEDPPD 14
||||| |||||||

DB 37 AAGEGPAHYEDPPD 50

RESULT 5

U13600
UDP-glucose 4-epimerase (EC 5.1.3.2) [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 19-Apr-2002
C:Accession: A13600

R:Delvecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
J.; Mazur, M.; Goldsman, E.; Selkov, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688

A:Accession: A13600
A:Molecule type: DNA

A:Residues: 1-328 <KUR>
A:Cross-references: GB:AE008918; PIDN:AAU53972.1; PID:g17984919; GSPDB:GN00191

A:Experimental source: strain 16M
C:Genetics:

A:Gene: BMEI10730
A:Map position: II

C:Superfamily: Escherichia coli UDP-glucose 4-epimerase; UDP-glucose 4-epimerase homology
C:Keywords: isomerase

Query Match

Best Local Similarity 56.4%; Score 44; DB 2; Length 328;
Pred. No. 8.5;

QY 1 AAGEGPAHYEDPPD 14
||||| |||||||

DB 2960 AAGEGPAHYEDPPD 49

Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAGEGPAHYEDPPD 12
||||| |||||||

DB 285 AAGEGPAHYEDPPD 295

RESULT 6

C72293
hypothetical protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 28-Jul-2000
C:Accession: C72293

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hlc
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: C72293
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-612 <ARN>

A:Cross-references: GB:AE001770; GB:AE000512; NID:94981658; PIDN:AAU56202.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:

A:Gene: TM1126
C:Superfamily: Thermotoga maritima hypothetical protein TM1126

Query Match
Best Local Similarity 55.8%; Score 43.5; DB 2; Length 612;
Pred. No. 21;

Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 AAGEGPAHYEDPPD 13
||||| |||||||

DB 224 AAGEGPAHYEDPPD 234

RESULT 7

S20473
fatty-acid synthase (EC 2.3.1.85) - Brevibacterium ammoniagenes

C:Species: Brevibacterium ammoniagenes
C>Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 05-May-2000
C:Accession: S20473; S28645

R:Meurer, G.; Biermann, G.; Schuetz, A.; Harth, S.; Schweizer, E.
Mol. Gen. Genet. 232, 106-116, 1992

A:Title: Molecular structure of the multifunctional fatty acid synthetase gene of Bre
he two yeast genes FAS1 and FAS2.

A:Reference number: S20473; MUID:92204122; PMID:1552898

A:Accession: S20473
A:Molecule type: DNA

A:Residues: 1-3104 <MEU>
A:Cross-references: EMBL:X64795

A:Gene: FAS
A:Start codon: GTG

C:Superfamily: Brevibacterium ammoniagenes fatty-acid synthase
C:Keywords: acyltransferase; coenzyme A

Query Match
Best Local Similarity 55.1%; Score 43; DB 2; Length 3104;
Pred. No. 1.6e+02;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAGEGPAHYEDPPD 14
||||| |||||||

DB 2960 AAGEGPAHYEDPPD 2973

A:Residues: 1-50, 'H', 52-318 <SEK>
 A:Cross-references: DDBJ:D13370; NID:9219473; PIDN:BA02633.1; PID:9219474
 R:Akiyama, K.; Seki, S.; Oshida, T.; Yoshida, M.C.
 Biochim. Biophys. Acta 1219, 15-25, 1994
 A:Title: Structure, promoter analysis and chromosomal assignment of the human APEX gene.
 A:Reference number: 547521; MUID:94368844; PMID:8086453
 A:Accession: 547521
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-147, 'E', 149-318 <AKT>
 A:Cross-references: DDBJ:D13370; NID:9219473; PIDN:BA02633.1; PID:9219474
 R:Harrierson, L.; Asclone, G.; Menninger, J.C.; Ward, D.C.; Dimple, B.
 Hum. Mol. Genet. 1, 677-680, 1992
 A:Title: Human apurinic endonuclease gene (APE): structure and genomic mapping (chromosome 10p11.23)
 A:Reference number: 139472; MUID:93258307; PMID:1284593
 A:Accession: 139472
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-146 <HAR>
 A:Cross-references: GB:M9703; NID:9178748; PIDN:AAA58373.1; PID:9553182
 R:Robson, C.N.; Hickson, I.D.
 Nucleic Acids Res. 19, 5519-5523, 1991
 A:Title: Isolation of cDNA clones encoding a human apurinic/apryimidinic endonuclease th
 A:Reference number: 534422; MUID:92051291; PMID:1719477
 A:Accession: 534422
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-236, 'A', 238-318 <RO2>
 A:Cross-references: EMBL:X5764; NID:932023; PIDN:CAA42437.1; PID:932024
 R:Dimple, B.; Herman, T.; Chen, D.S.
 Proc. Natl. Acad. Sci. U.S.A. 88, 11450-11454, 1991
 A:Title: Cloning and expression of APE, the cDNA encoding the major human apurinic endo
 A:Reference number: A41631; MUID:92107968; PMID:1722334
 A:Accession: A41631
 A:Molecule type: mRNA
 A:Residues: 1-56, 'A', 58-305, 'A', 307-318 <DEM1>
 A:Cross-references: GB:M80261; NID:9178742; PIDN:AAA58371.1; PID:9178743
 A:Accession: B41631
 A:Molecule type: protein
 A:Residues: 2-21, 'P', 23-26 <DEM2>
 R:Barzilai, G.; Walker, L.J.; Robson, C.N.; Hickson, I.D.
 Nucleic Acids Res. 23, 1544-1550, 1995
 A:Title: Site-directed mutagenesis of the human DNA repair enzyme HAP1: identification c
 A:Reference number: S55547; MUID:95303638; PMID:7784208
 A:Accession: S55547
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 62-318 <BAR>
 C:Genetics:
 A:Gene: GDB:APX; ref-1; HAP1
 A:Cross-references: GDB:129088; OMIM:107748
 A:Map position: 14q11.2-14q12
 A:Introns: 20/1; 82/3; 147/1
 A:Note: The list of introns may be incomplete
 C:Function:
 A:Description: catalyzes endonucleolytic cleavage near apurinic or apyrimidinic sites to
 A:Pathway: DNA repair
 C:Superfamily: exodeoxyribonuclease III
 C:Keywords: carbon-oxygen lyase; DNA repair; endonuclease; magnesium; nucleus
 F:2-318/Product: DNA (apurinic or apyrimidinic site) lyase I #status experimental <MAT>
 F:96/Binding site: magnesium (Glu) #status predicted
 F:309/Active site: His #status predicted

Query Match 100.0%; Score 78; DB 2; Length 318;
 Best Local Similarity 100.0%; Pred. No. 1.2e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEPALYEDPPD 14
 |||||
 DB 37 AAGEPALYEDPPD 50

RESULT 2

S42397
 DNA (apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - rat
 N:Alternate names: apurinic/apryimidinic endonuclease
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Oct-1994 #sequence, revision 10-Nov-1995 #text, change 18-Feb-2000
 C:Accession: 542397
 R:Willson, T.M.; Carney, J.P.; Kelley, M.R.
 Nucleic Acids Res. 22, 530-531, 1994
 A:Title: Cloning of the multifunctional rat apurinic/apryimidinic endonuclease (RAPEN
 A:Reference number: 542397; MUID:94173705; PMID:7510394
 A:Accession: 542397
 A:Molecule type: mRNA
 A:Residues: 1-316 <WIL>
 A:Cross-references: GB:L27076; NID:9468370; PIDN:AAA21019.1; PID:9468371
 C:Superfamily: exodeoxyribonuclease III
 C:Keywords: carbon-oxygen lyase; DNA repair; endonuclease; nucleus

Query Match 94.9%; Score 74; DB 2; Length 316;
 Best Local Similarity 92.9%; Pred. No. 5.8e-05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGEPALYEDPPD 14
 |||||
 DB 35 AAGEPALYEDPPD 48

RESULT 3
 A39500
 DNA (apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - mouse
 N:Alternate names: apurinic/apryimidinic endonuclease; deoxyribonuclease
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence, revision 30-Jun-1992 #text, change 20-Jun-2000
 C:Accession: A39500; S17524; A56747; I49098; J00372
 R:Seki, S.; Akiyama, K.; Watanabe, S.; Hattushika, M.; Ikeda, S.; Tsutsui, K.
 J. Biol. Chem. 266, 20797-20802, 1991
 A:Title: cDNA and deduced amino acid sequence of a mouse DNA repair enzyme (APEX nucl
 A:Reference number: A39500; MUID:92041936; PMID:1939131
 A:Accession: A39500
 A:Molecule type: mRNA
 A:Residues: 1-317 <SEK>
 A:Cross-references: GB:D90374; NID:9220336; PIDN:BA01382.1; PID:9220337
 A:Note: Part of this sequence, including the amino end of the mature protein, was con
 R:Seki, S.; Ikeda, S.; Watanabe, S.; Hattushika, M.; Tsutsui, K.; Akiyama, K.; Zhang,
 Biochim. Biophys. Acta 1079, 57-64, 1991
 A:Title: A mouse DNA repair enzyme (APEX nuclease) having exonuclease and apurinic/cp
 A:Reference number: S17524; MUID:91363416; PMID:1716153
 A:Accession: S17524
 A:Molecule type: protein
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 2-18, 'xxx', 22 <SE2>
 R:Akiyama, K.; Nagao, K.; Oshida, T.; Tsutsui, K.; Yoshida, M.C.; Seki, S.
 Genomics 26, 63-69, 1995
 A:Title: Cloning, sequence analysis, and chromosomal assignment of the mouse Apex gen
 A:Reference number: A56747; MUID:95301294; PMID:7782087
 A:Accession: A56747
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-18 <AKT>
 A:Cross-references: GB:D38077
 R:Takiguchi, Y.; Chen, D.J.
 Mamm. Genome 5, 717-722, 1994
 A:Title: Genomic structure of the mouse apurinic/apryimidinic endonuclease gene.
 A:Reference number: I49098; MUID:95178846; PMID:7533013
 A:Accession: I49098
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <RES>
 A:Cross-references: EMBL:U12273; NID:9533107; PIDN:AA013769.1; PID:9533108
 C:Genetics:
 A:Gene: MGI:Apex
 A:Cross-references: MGI:88042
 A:Introns: 19/1; 81/3; 146/1
 C:Superfamily: exodeoxyribonuclease III

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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:36:28 ; Search time 16 seconds
(without alignments)
84.118 Million cell updates/sec

Title: US-10-001-426-2
Perfect score: 78
Sequence: 1 AAGGCPALYEDPPD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	78	100.0	318	2	S23550	DNA-(apurinic or a
2	74	94.9	316	2	S42397	DNA-(apurinic or a
3	74	94.9	317	2	A39500	DNA-(apurinic or a
4	62	79.5	318	2	S26830	DNA-(apurinic or a
5	44	56.4	328	2	A13600	UDPglucose 4-epime
6	43.5	55.8	612	2	C72293	hypothetical prote
7	43	55.1	3104	2	S20473	fatty-acid synthas
8	42	53.8	303	2	T42699	hypothetical prote
9	42	53.8	1153	2	A49676	nitric-oxide synth
10	42	53.8	1182	2	I48378	hairless protein -
11	42	53.8	1453	2	F88640	protein F52C12.4 l
12	41	52.6	126	2	A84567	hypothetical prote
13	41	52.6	293	2	AP0617	probable DNA methy
14	41	52.6	1144	1	A43271	nitric-oxide synth
15	41	52.6	1147	1	S47647	nitric-oxide synth
16	41	52.6	1147	1	I56575	nitric-oxide synth
17	41	52.6	1147	1	S38253	nitric-oxide synth
18	41	52.6	1147	1	I53165	nitric-oxide synth
19	41	52.6	1147	1	JC5027	nitric-oxide synth
20	41	52.6	1147	2	JC5028	nitric-oxide synth
21	41	52.6	1147	2	JC5029	nitric-oxide synth
22	41	52.6	1147	2	S65440	nitric-oxide synth
23	40	51.3	95	2	S36634	nitric-oxide synth
24	40	51.3	201	2	H70615	hypothetical prote
25	40	51.3	219	2	A45384	GTP-binding protei
26	40	51.3	369	2	T46950	probable ATPase co
27	40	51.3	450	2	DB7342	multidrug resistan
28	40	51.3	586	2	A43675	capsid protein p40
29	40	51.3	646	2	T28868	hypothetical prote

30	40	51.3	687	2	H72485
31	40	51.3	825	2	A48537
32	40	51.3	924	2	E87092
33	40	51.3	953	2	B70681
34	40	51.3	987	2	G98211
35	40	51.3	987	2	AB3075
36	40	51.3	1094	2	C59434
37	40	51.3	1123	2	A72311
38	40	51.3	1354	2	T13930
39	39	50.0	138	2	S24107
40	39	50.0	241	2	C82852
41	39	50.0	267	2	B84089
42	39	50.0	268	2	F70823
43	39	50.0	608	2	I53269
44	39	50.0	717	1	HHF83
45	39	50.0	4077	2	T17484

ALIGNMENTS

RESULT 1
DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) 1 precursor - human
N:Alternate names: Ap endonuclease 1 (Apen); APL; APEX nuclease; apurinic/aprimidini
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence revision 10-Nov-1995 #text change 20-Jun-2000
C:Accession: S23550; S25570; S35456; S23935; S47521; I39472; S34422; A41631;
R:Xanthoudakis, S.; Miao, G.; Wang, F.; Fan, Y.C.E.; Curran, T.
EMBO J. 11, 3323-3335, 1992
A:Title: Redox activation of Fos-Jun DNA binding activity is mediated by a DNA repair
A:Reference number: S23550; MUID:92371440; PMID:1380454
A:Accession: S23550
A:Molecule type: mRNA; protein
A:Residues: 1-318 <XAN>
A:Cross-references: GB:S43127; NID:9254068; PIDN:AA822977.1; PID:9254069
A:Note: part of this sequence, including the amino end of the mature protein, was det
R:Robson, C.N.; Hochhauser, D.; Gray, R.; Rack, K.; Buckle, V.J.; Hickson, I.D.
Nucleic Acids Res. 20, 4417-4421, 1992
A:Title: Structure of the human DNA repair gene HAP1 and its localisation to chromoso
A:Reference number: S25570; MUID:93027134; PMID:1383925
A:Accession: S25570
A:Molecule type: DNA
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-318 <ROB>
A:Cross-references: EMBL:X66133; NID:932021; PIDN:CAA6925.1; PID:932022
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1992
R:Cheng, X.B.; Bunville, J.; Patterson, T.A.
Nucleic Acids Res. 20, 370, 1992
A:Title: Nucleotide sequence of a cDNA for an apurinic/aprimidinic endonuclease from
A:Reference number: S35454; MUID:92158631; PMID:1371347
A:Accession: S35454
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-318 <CH>
A:Cross-references: EMBL:M81955; NID:9178746; PIDN:AAA58372.1; PID:9178747
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R:Zhao, B.; Grandy, D.K.; Hagerup, J.M.; Magenis, R.E.; Smith, L.; Chauman, B.C.; Hen
Nucleic Acids Res. 20, 4097-4098, 1992
A:Title: The human gene for apurinic/aprimidinic endonuclease (HAP1): sequence and
A:Reference number: S35456; MUID:92375705; PMID:1380694
A:Accession: S35456
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-318 <HAP>
A:Cross-references: EMBL:M92444; NID:9183779; PIDN:AAA56629.1; PID:9183780
R:Seiki, S.; Hattushika, M.; Watanabe, S.; Akiyama, K.; Nagao, K.; Tsutsui, K.
Biochim. Biophys. Acta 1131, 287-299, 1992
A:Title: CDNA cloning, sequencing, expression and possible domain structure of human
A:Reference number: S23935; MUID:92329542; PMID:1627644
A:Accession: S23935
A:Status: preliminary
A:Molecule type: mRNA

probable hydantoin
starch branching e
probable ribonucle
probable rne prote
hypothetical prote
sarcosine oxidase
KIAA1688 protein l
conserved hypotet
tripeptidyl-peptid
envelope protein -
competence protein
hypothetical prote
hypothetical prote
prolactin receptor
heat shock protein
hypothetical prote

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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:23:53 : Search time 11 Seconds

(without alignments)
52.788 Million cell updates/sec

Title: US-10-001-426-2

Sequence: 1 AAGECPALVEDPPD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	100.0	317	1	PEP1_HUMAN
2	74	94.9	316	1	PEP1_MOUSE
3	74	94.9	316	1	PEP1_RAT
4	62	79.5	317	1	PEP1_BOVIN
5	42	53.8	215	1	NOS2_PTC
6	42	53.8	679	1	TKT1_KTOLA
7	42	53.8	746	1	STM2_HUMAN
8	42	53.8	1149	1	NS2_CAVPO
9	42	53.8	1153	1	NS2A_HUMAN
10	42	53.8	1181	1	HAIR_RAT
11	42	53.8	1182	1	HAIR_MOUSE
12	41	52.6	130	1	EXR3_ARATH
13	41	52.6	1144	1	NOS2_MOUSE
14	41	52.6	1147	1	NOS2_RAT
15	41	52.6	1147	1	NS2D_HUMAN
16	40	51.3	209	1	CCX1_HUMAN
17	40	51.3	219	1	RB3D_MOUSE
18	40	51.3	219	1	RB3D_RAT
19	40	51.3	586	1	VP40_ILVT
20	40	51.3	591	1	NOS2_CANFA
21	40	51.3	733	1	HIC1_HUMAN
22	40	51.3	892	1	HIC1_MOUSE
23	40	51.3	987	1	SOXA_RHME
24	39.5	50.6	561	1	KCN1_HUMAN
25	39	50.0	268	1	Y739_MYCTU
26	39	50.0	351	1	KLF2_RAT
27	39	50.0	354	1	KLF2_MOUSE
28	39	50.0	608	1	PRLR_MOUSE
29	39	50.0	716	1	HS83_DROAV
30	39	50.0	717	1	HS83_DROME
31	39	50.0	841	1	AXN_CHICK
32	39	50.0	857	1	DD24_MOUSE
33	38	48.7	390	1	UGAT_MOUSE

ALIGNMENTS

RESULT 1	APPEL_HUMAN	STANDARD:	PRT:	317 AA.
AC	P27655; Q99775; Q969L5;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP			
DE	endonuclease 1) (APEX nuclease) (APEN) (REF-1 protein).			
GN	APEX OR APE OR HAP1 OR REPI OR APX.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93027134; PubMed=1383925;			
RA	Robson C.N., Hochhauser D., Craig R., Rack K., Buckle I.D.,			
RA	Hickson I.D.;			
RT	"Structure of the human DNA repair gene HAP1 and its localisation to			
RT	chromosome 14q 11.2-12.";			
RL	Nucleic Acids Res. 20:4417-4421(1992).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Melanocyte;			
RX	MEDLINE=92051291; PubMed=1719477;			
RA	Robson C.N., Hickson I.D.;			
RT	"Isolation of cDNA clones encoding a human apurinic/aprimidinic			
RT	endonuclease that corrects DNA repair and mutagenesis defects in E.			
RT	coli xth (exonuclease III) mutants.";			
RL	Nucleic Acids Res. 19:5519-5523(1991).			
RL	[3]			
RP	SEQUENCE FROM N.A. AND SEQUENCE OF 1-20.			
RX	MEDLINE=92371440; PubMed=1380454;			
RA	Xanthoudakis S., Mao G., Wang F., Pan Y.-C.E., Curran T.;			
RT	"Redox activation of Fos-Jun DNA binding activity is mediated by a			
RT	DNA repair enzyme.";			
RL	EMBO J. 11:3323-3335(1992).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92375705; PubMed=1380694;			
RA	Zhao B., Grandy D.K., Hagerup J.M., Magenis R.E., Smith L.,			
RA	Chauban B.C., Henner W.D.;			
RT	"The human gene for apurinic/aprimidinic endonuclease (HAP1):			
RT	sequence and localization to chromosome 14 band q12.";			
RL	Nucleic Acids Res. 20:4097-4098(1992).			
RL	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92329542; PubMed=1627644;			
RA	Seki S., Hatsuoka M., Watanabe S., Akiyama K., Nagao K., Tsutsui K.;			
RT	"cDNA cloning, sequencing, expression and possible domain structure			
RT	of human APEX nuclease homologous to Escherichia coli exonuclease			
RT	III.";			
RL	Biochim. Biophys. Acta 1131:287-299(1992).			
RL	[6]			
RP	SEQUENCE FROM N.A.			

34	38	48.7	446	1	HOSM_YARLI
35	38	48.7	456	1	GLMT_ECOLI
36	38	48.7	456	1	GLMT_HAEIN
37	38	48.7	576	1	ACH2_DROME
38	38	48.7	933	1	PRGR_HUMAN
39	38	48.7	1111	1	GLI1_MOUSE
40	38	48.7	1136	1	NOS2_CHICK
41	38	48.7	1332	1	PUR4_XYLA
42	38	48.7	1447	1	DCC_HUMAN
43	38	48.7	1447	1	DCC_MOUSE
44	37	47.4	198	1	RB16_RAT
45	37	47.4	296	1	Y121_HUMAN

012726	yarrowia 11
P17114	escherichia
P43889	haemophilus
P17644	drosophila
P06401	homo sapien
P47806	mus musculu
Q90703	gallus galli
Q96d66	xyloella fas
P43146	homo sapien
P70211	mus musculu
P35291	rattus norv
Q14335	homo sapien

RX MEDLINE-94368844; PubMed-8086453;
 RA Akiyama K., Seki S., Oshida T., Yoshida M.;
 RT "Structure, promoter analysis and chromosomal assignment of the human
 RT Apex gene.";
 RL Biochim. Biophys. Acta 1219:15-25(1994).
 RN [77]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-92107968; PubMed-1722334;
 RT Demple B., Herman T., Chen D.S.;
 RT "Cloning and expression of APE, the cDNA encoding the major human
 RT apurinic endonuclease: definition of a family of DNA repair
 RT enzymes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:11450-11454(1991).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92158631; PubMed-1371347;
 RA Cheng X.B., Bunville J., Patterson T.A.;
 RT "Nucleotide sequence of a cDNA for an apurinic/aprimidinic
 RT endonuclease from HeLa cells.";
 RL Nucleic Acids Res. 20:370-370(1992).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE-97264341; PubMed-9110174;
 RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
 RA Ricardente J.T., Wentland K.A., Lennon G., Gibbs R.A.;
 RT "Large-scale concatenation cDNA sequencing.";
 RL Genome Res. 7:353-358(1997).
 RN [10]
 RP SEQUENCE FROM N.A., AND VARIANT GIU-147.
 RC TISSUE-Brain, Lung, and Skin;
 RA Strausberg R.;
 RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL [11]
 RP SEQUENCE OF 1-145 FROM N.A.
 RC TISSUE-Placenta;
 RX MEDLINE-93258307; PubMed-1284593;
 RA Harrison L., Ascione G., Menninger J.C., Ward D.C., Demple B.;
 RT "Human apurinic endonuclease gene (APE): structure and genomic
 RT mapping (chromosome 14q11.2-12).";
 RL Hum. Mol. Genet. 1:677-680(1992).
 RN [12]
 RP MUTAGENESIS OF ASN-211.
 RX MEDLINE-97086686; PubMed-8932375;
 RA Rothwell D.G., Hickson I.D.;
 RT "Asparagine 212 is essential for abasic site recognition by the human
 RT DNA repair endonuclease HAP1.";
 RL Nucleic Acids Res. 24:4217-4221(1996).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
 RX MEDLINE-21184546; PubMed-11286553;
 RA Beerlink P.T., Segelke B.W., Hadi M.Z., Erzberger J.P.,
 RA Wilson D.M. III, Rupp B.;
 RT "Two divalent metal ions in the active site of a new crystal form of
 RT human apurinic/aprimidinic endonuclease, apei: implications for the
 RT catalytic mechanism.";
 RL J. Mol. Biol. 307:1023-1034(2001).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 31-317.
 RX MEDLINE-98063001; PubMed-9351835;
 RA Gorman M.A., Morera S., Rothwell D.G., de la Fortelle E., Mol C.D.,
 RA Tainer J.A., Hickson I.D., Freemont P.S.;
 RT "The crystal structure of the human DNA repair endonuclease HAP1
 RT suggests the recognition of extra-helical deoxyribose at DNA abasic
 RT sites.";
 RL EMBO J. 16:6548-6558(1997).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-317.
 RX MEDLINE-20129262; PubMed-10667800;
 RA Mol C.D., Izumi T., Mitra S., Tainer J.A.;
 RT "DNA-bound structures and mutants reveal abasic DNA binding by APE1
 RT DNA repair and coordination.";

RL Nature 403:451-456(2000).
 CC -1- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
 CC IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
 CC REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
 CC BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
 CC -1- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
 CC leaving a 3'-terminal unsaturated sugar and a product with a
 CC terminal 5'-phosphate.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE AP/EXO FAMILY OF DNA REPAIR ENZYMES.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X66133; CAA46925.1; -
 CC EMBL: X59764; CAA42437.1; -
 CC EMBL: M92444; AAA58629.1; -
 CC EMBL: M99703; AAA58373.1; -
 CC EMBL: D90373; BAA14381.1; -
 CC EMBL: D13370; BAA02633.1; -
 CC EMBL: M80261; AAA58371.1; -
 CC EMBL: M81955; AAA58372.1; -
 CC EMBL: U79268; AAB50212.1; -
 CC EMBL: BC002338; AAH02338.1; -
 CC EMBL: BC004979; AAH04979.1; -
 CC EMBL: BC008145; AAH08145.1; -
 CC EMBL: BC019291; AAH19291.1; -
 CC EMBL: S43127; AAB22977.1; -
 CC PIR: A41631; A41631.
 CC PIR: JU0373; JU0373.
 CC PIR: S22072; S22072.
 CC PIR: S23550; S23550.
 CC PIR: S23935; S23935.
 CC PIR: S25570; S25570.
 CC PIR: S35456; S35456.
 CC PIR: S35454; S35454.
 CC PDB: 1BX; 22-JUN-99.
 CC PDB: 1E9N; 16-FEB-01.
 CC PDB: 1HD7; 16-FEB-01.
 CC PDB: 1DE8; 02-FEB-00.
 CC PDB: 1DE9; 02-FEB-00.
 CC PDB: 1DEW; 02-FEB-00.
 CC TRANSFAC: T04878; -
 CC GeneW: HGNC:587; APEX.
 CC MIM: 107748; -
 CC InterPro: IPR000097; Apendonclase.
 CC InterPro: IPR004442; Exonase_III.
 CC InterPro: IPR004808; ExoIII_xth.
 CC InterPro: IPR005135; Exo_endo_phos.
 CC Pfam: PF03372; Exo_endo_phos; 1.
 CC TIGRfam: TIGR00195; exonase_III; 1.
 CC TIGRfam: TIGR00633; xth; 1.
 CC PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.
 CC PROSITE: PS00727; AP_NUCLEASE_F1_2; 1.
 CC PROSITE: PS00728; AP_NUCLEASE_F1_3; 1.
 CC DNA repair; Lyase; Nuclear protein; Polymorphism; 3D-structure.
 CC INIT_MET 0 0
 CC METAL 67 67 MAGNESIUM OR MANGANESE.
 CC METAL 95 95 MAGNESIUM OR MANGANESE.
 CC METAL 209 209 MAGNESIUM OR MANGANESE.
 CC METAL 211 211 MAGNESIUM OR MANGANESE.
 CC METAL 307 307 MAGNESIUM OR MANGANESE.
 CC METAL 308 308 MAGNESIUM OR MANGANESE.
 CC ACT_SITE 308 308 GENERAL BASE (BY SIMILARITY).
 CC VARIANT 50 50 O -> H (IN DBSNP:1048945).
 CC /FTId=VAR_013455.

Query Match 100.0%: Score 78: DB 1: Length 317;
 Best Local Similarity 100.0%: Pred. No. 6.3e-06;
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

OY 1 AAGEGPALYEDPPD 14
 DB 36 AAGEGPALYEDPPD 49

RESULT 2
 APEL_MOUSE STANDARD: PRT: 316 AA.
 AC P28352:
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
 endonuclease 1) (APEX nuclease) (APEN).
 GN APEX OR APE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-92041936; PubMed-1939131;
 RA Seki S., Akiyama K., Watanabe S., Hatushika M., Ikeda S.,
 RA Tsutsui K.;
 RT "cDNA and deduced amino acid sequence of a mouse DNA repair enzyme
 (APEX nuclease) with significant homology to Escherichia coli
 exonuclease III".
 RT J. Biol. Chem. 266:20797-20802(1991).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-129; TISSUE=Embryo;
 RA MEDLINE-95178846; PubMed-7533013;
 RA Takiguchi Y., Chen D.J.;
 RT "Genomic structure of the mouse apurinic/apyrimidinic endonuclease
 gene".
 RT Mamm. Genome 5:717-722(1994).
 RL [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=Blood;
 RA MEDLINE-95301294; PubMed-7782087;
 RA Akiyama K., Nagao K., Oshida T., Tsutsui K., Yoshida M.C., Seki S.;
 RT "Cloning, sequence analysis, and chromosomal assignment of the mouse
 Apex gene".
 RT Genomics 26:63-69(1995).
 RL [4]
 RN PARTIAL SEQUENCE OF 1-21, AND CHARACTERIZATION.
 RP TISSUE=Ascites;
 RA MEDLINE-91163416; PubMed-1716153;
 RA Seki S., Ikeda S., Watanabe S., Hatushika M., Tsutsui K., Akiyama K.,
 RA Zhang B.;
 RT "A mouse DNA repair enzyme (APEX nuclease) having exonuclease and
 apurinic/apyrimidinic endonuclease activities: purification and
 characterization".
 RT Biochim. Biophys. Acta 1079:57-64(1991).
 CC -1- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
 IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
 CC REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
 CC BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
 CC -1- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
 CC leaving a 3'-terminal unsaturated sugar and a product with a
 CC terminal 5'-phosphate.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE AP/EXO FAMILY OF DNA REPAIR ENZYMES.
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 CC -----

DR EMBL: D90374; BAA14382.1; -;
 DR EMBL: U12273; AAC13769.1; -;
 DR EMBL: D38077; BAA07270.1; -;
 DR PIR: S17524; S17524.
 DR PIR: A39500; A39500.
 DR HSSP: P27695; 1BX.
 DR MGD: MG1:88042; Apex.
 DR InterPro: IPR000097; APendonc1se1.
 DR InterPro: IPR004442; EXODNase_III.
 DR InterPro: IPR004808; EXOIII_xth.
 DR Pfam: PF03372; Exo_endo_phos. 1.
 DR TIGRFAMS: TIGR00195; exoDNase_III; 1.
 DR TIGRFAMS: TIGR00633; xth; 1.
 DR PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.
 DR PROSITE: PS00727; AP_NUCLEASE_F1_2; 1.
 DR PROSITE: PS00728; AP_NUCLEASE_F1_3; 1.
 KW DNA repair; Lyase; Nuclear protein.
 FT INIT_MET 0
 FT METAL 66
 FT METAL 66
 FT METAL 94
 FT METAL 208
 FT METAL 210
 FT METAL 306
 FT METAL 307
 FT SITE 210
 FT ACT_SITE 307
 FT SQ SEQUENCE 316 AA; 35359 MW; CF899FEA8182AA558 CRC64;
 Query Match 94.9%: Score 74: DB 1: Length 316;
 Best Local Similarity 92.9%: Pred. No. 3e-05;
 Matches 13: Conservative 0: Mismatches 1: Indels 0: Gaps 0;

OY 1 AAGEGPALYEDPPD 14
 DB 35 AAGEGPALYEDPPD 48

RESULT 3
 APEL_RAT STANDARD: PRT: 316 AA.
 AC P43138:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
 endonuclease 1) (APEX nuclease) (APEN).
 GN APEX OR APE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Testis;
 RA MEDLINE-94173709; PubMed-7510394;
 RA Wilson T.M., Carney J.P., Kelley M.R.;
 RT "Cloning of the multifunctional rat apurinic/apyrimidinic
 RT endonuclease (APEN)/Redox factor from an immature T cell line".
 RL Nucleic Acids Res. 22:530-531(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE=Brain;
 RA Tan Y., Akiyama K., Seki S., Tabayashi T., Tanigawa M.;
 RL Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.
 RN [3]

SEQUENCE FROM N.A.
 RA Yao M., Akiyama K., Tan Y., Sarker A.H., Ikeda S., Alam S.S.,
 RA Tetsui K., Yoshida M.C., Seki S.,
 RT "Genomic structure of the rat Apex (major AP endonuclease) gene with
 RT an adjacent putative O-sialoglycoproteinase (Prsmgl/Gcp11) gene and a
 RT processed pseudogene (Apexpl).";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
 CC IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
 CC REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
 CC BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
 CC -1- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
 CC leaving a 3'-terminal unsaturated sugar and a product with a
 CC terminal 5'-phosphate.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE AP/EXO A FAMILY OF DNA REPAIR ENZYMES.

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 CC EMBL: L27076; AAA21019.1; -;
 CC EMBL: D44495; BA07938.1; -;
 CC EMBL: AB023065; BA082124.1; -;
 CC HSSP: P27695; 1BX.
 CC InterPro: IPR000097; Appendoc1sel.
 CC InterPro: IPR004442; ExoDNase_III.
 CC InterPro: IPR004808; ExoIII_xch.
 CC InterPro: IPR005135; Exo_endo_phos.
 CC Pfam: PF03372; Exo_endo_phos; 1.
 CC TIGRfams: TIGR00195; exoDNase_III; 1.
 CC TIGRfams: TIGR00633; xth; 1.
 CC PROSITE: PS00726; AP_NUCLEASE_FL_1; 1.
 CC PROSITE: PS00727; AP_NUCLEASE_FL_2; 1.
 CC PROSITE: PS00728; AP_NUCLEASE_FL_3; 1.
 CC DNA repair; Lyase; Nuclear protein.
 CC INIT MET 0
 CC METAL 66 66 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 94 94 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 208 208 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 210 210 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 306 306 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 307 307 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC ACT SITE 307 307 GENERAL BASE (BY SIMILARITY).
 CC CONFLICT 9 9 MISSING (IN REF. 1).
 CC CONFLICT 235 235 R -> A (IN REF. 1).
 CC CONFLICT 287 287 H -> Q (IN REF. 1).
 CC SEQUENCE 316 AA; 35407 MW; FB27D005917C4116 CRC64;

 CC Query Match 94.9%; Score 74; DB 1; Length 316;
 CC Best Local Similarity 92.9%; Pred. No. 3e-05;
 CC Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGEGALYEDPPD 14
 DB 35 AAGEGALYEDPPD 48

RESULT 4
 ID APEL_BOVIN STANDARD; PRT; 317 AA.
 AC P23196;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) (AP
 DE endonuclease 1) (APEX nuclease) (APEN).

APEX OR APE OR BAP1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.
 RC TISSUE=Thymus;
 RX MEDLINE=91212169; PubMed=1708495;
 RA ROBINSON C.N., Milne A.M., Pappin D.J.C., Hickson I.D.;
 RT "Isolation of cDNA clones encoding an enzyme from bovine cells that
 RT repairs oxidative DNA damage in vitro: homology with bacterial repair
 RT enzymes";
 RL Nucleic Acids Res. 19:1087-1092(1991).
 CC [2]
 CC SEQUENCE OF 1-22.
 RC TISSUE=Thymus;
 RX MEDLINE=87289027; PubMed=2441359;
 RA Henner W.D., Kiker N.P., Jorgensen T.J., Munck J.-N.;
 RT "Purification and amino-terminal amino acid sequence of an
 RT apurinic/aprimidinic endonuclease from calf thymus";
 RL Nucleic Acids Res. 15:5529-5544(1987).
 CC -1- FUNCTION: REPAIRS OXIDATIVE DNA DAMAGES IN VITRO. MAY HAVE A ROLE
 CC IN PROTECTION AGAINST CELL LETHALITY AND SUPPRESSION OF MUTATIONS.
 CC REMOVES THE BLOCKING GROUPS FROM THE 3' TERMINI OF THE DNA STRAND
 CC BREAKS GENERATED BY IONIZING RADIATIONS AND BLEOMYCIN.
 CC -1- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
 CC leaving a 3'-terminal unsaturated sugar and a product with a
 CC terminal 5'-phosphate.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: THYMUS.
 CC -1- INDUCTION: BY SEVERAL DNA DAMAGING AGENTS.
 CC -1- SIMILARITY: BELONGS TO THE AP/EXO A FAMILY OF DNA REPAIR ENZYMES.

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 CC EMBL: X56685; CAA40014.1; -;
 CC PIR: S26830; S26830.
 CC HSSP: P27695; 1HD7.
 CC InterPro: IPR000097; Appendoc1sel.
 CC InterPro: IPR004442; ExoDNase_III.
 CC InterPro: IPR004808; ExoIII_xch.
 CC InterPro: IPR005135; Exo_endo_phos.
 CC Pfam: PF03372; Exo_endo_phos; 1.
 CC TIGRfams: TIGR00195; exoDNase_III; 1.
 CC TIGRfams: TIGR00633; xth; 1.
 CC PROSITE: PS00726; AP_NUCLEASE_FL_1; 1.
 CC PROSITE: PS00727; AP_NUCLEASE_FL_2; 1.
 CC PROSITE: PS00728; AP_NUCLEASE_FL_3; 1.
 CC DNA repair; Lyase; Nuclear protein.
 CC INIT MET 0
 CC METAL 67 67 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 95 95 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 209 209 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 211 211 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 307 307 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC METAL 308 308 MAGNESIUM OR MANGANESE (BY SIMILARITY).
 CC ACT SITE 308 308 GENERAL BASE (BY SIMILARITY).
 CC CONFLICT 20 21 PE -> LP (IN REF. 2).
 CC SEQUENCE 317 AA; 35438 MW; 58A7B2029B0891B4 CRC64;

 CC Query Match 79.5%; Score 62; DB 1; Length 317;
 CC Best Local Similarity 78.6%; Pred. No. 0.0033;
 CC Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 AGECPALYEDPPD 14
 DB 36 AVEGAVLYEDPPD 49

RESULT 5

NOS2_PIG STANDARD: PRT: 215 AA.

AC P79290: 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 GN NOS2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;

NCBI_TaxID=9823;

SEQUENCE FROM N.A.

TISSUE=Spleen;
 MEDLINE=98273497; PubMed=9613441;

Pampusch M.S., Bennis A.M., Harsch S., Murtough M.P.;
 Vet. Immunol. Immunopathol. 61:279-289(1998).

Inducible nitric oxide synthase expression in porcine immune cells.;
 - FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE

WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.

- 1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) -> citrulline +

nitric oxide + N NADP(+).

- 1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES

TERPAHYDROBIOTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF

THE ENZYME (BY SIMILARITY).

- 1- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN (BY

SIMILARITY).

- 1- SUBUNIT: HOMODIMER (BY SIMILARITY).

- 1- TISSUE SPECIFICITY: DETECTED IN BOTH STIMULATED AND UNSTIMULATED

IMMUNE CELLS AND MACROPHAGES WITH LITTLE OR NO UPREGULATION

FOLLOWING CELLULAR STIMULATION WITH LIPOPOLYSACCHARIDES (LPS) OR

CONCANAVALIN A (CONA).

- 1- INDUCTION: LITTLE BY LPS OR CONA IN SPLEEN CELLS.

- 1- SIMILARITY: BELONGS TO THE NOS FAMILY.

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CC -----

CC EMBL: U59390; AAB40614.1; -.

DR HSSP: P35228; 4NOS.

DR InterPro: IPR004030; NO_synthase.

DR Pfam: PF02898; NO_synthase; 1.

DR PROSITE: PS60001; NOS: PARTIAL.

KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;

KW Multigene family.

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

FT NON_TER 1 215

TKT1_KIULA STANDARD: PRT: 679 AA.
 AC 012630: 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Transketolase (EC 2.2.1.1) (TK).

GN TKT1.

OS Kluyveromyces fragilis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

OX NCBI_TaxID=28985;

NCBI_TaxID=28985;

SEQUENCE FROM N.A.

STRAIN=CBS 2359/152;

MEDLINE=97153463; PubMed=9000376;

RA Jacoby J.J., Hehlisch J.J.;

"Analysis of a transketolase gene from Kluyveromyces fragilis reveals

that the yeast enzymes are more related to transketolases of

prokaryotic origins than to those of higher eukaryotes.";

RL Curr. Genet. 31:15-21(1997).

- 1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde

3-phosphate -> D-ribose 5-phosphate + D-xylulose 5-phosphate.

- 1- COFACTOR: THIAMINE PYROPHOSPHATE.

- 1- SUBUNIT: HOMODIMER (BY SIMILARITY).

- 1- SIMILARITY: BELONGS TO THE TRANSKETOLASE FAMILY.

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CC -----

CC EMBL: U65983; AAB05935.1; -.

DR HSSP: P23254; 1TKR.

DR InterPro: IPR000360; Transketolase.

DR Pfam: PF00456; Transketolase; 1.

DR Pfam: PF02779; transketolase; 1.

DR Pfam: PF02780; transketolase; 1.

DR TIGRfam: TIGR00232; tktlase; 1.

DR PROSITE: PS00801; TRANSKETOLASE; 1.

DR PROSITE: PS00802; TRANSKETOLASE; 2; 1.

KW Transferrase; Thiamine pyrophosphate.

SEQUENCE 679 AA; 73703 MW; BC5F3C61A78CD4A CRC64;

Query Match 53.8%; Score 42; DB 1; Length 679;

Best Local Similarity 70.0%; Pred. No. 19;

Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGECPALYE 10

DB 637 ASGCPAYVE 646

1:1:1:1:1:1

STW2_HUMAN STANDARD: PRT: 746 AA.

AC Q9P246; Q9P246; Q9H8R1;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Stromal interaction molecule 2 precursor.

GN STW2 OR KIAA1482.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

NCBI_TaxID=9606;

SEQUENCE FROM N.A., SEQUENCE OF 15-24, SUBUNIT, GLYCOSYLATION,

PHOSPHORYLATION, AND TISSUE SPECIFICITY.

RESULT 6

RX MEDLINE=21356314; PubMed=11463338;
 RA Williams R.T., Manji S.S.M., Parker N.J., Hancock M.S.,
 RA Van Stekelenburg L., Eid J.-P., Senior P.V., Kazenwadel J.S.,
 RA Shandela T., Saint R., Smith P.J., Dziadek M.A.;
 RT "Identification and characterization of the STM (stromal interaction
 RT molecule) gene family: coding for a novel class of transmembrane
 RT proteins";
 RL Biochem. J. 357:673-685(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20277482; PubMed=10819331;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human
 RT genes. XVII. The complete sequences of 100 new cDNA clones from brain
 RT which code for large proteins in vitro.";
 RL DNA Res. 7:143-150(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Amygdala;
 RX MEDLINE=21154917; PubMed=11230166;
 RA Wiemann S., Weill B., Wellenreuther R., Gassenhuber J., Glassl S.,
 RA Ansgere W., Boecher M., Bloecher H., Bauersachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koehler K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs.";
 RL Genome Res. 11:422-435(2001).
 RN [4]
 RP SEQUENCE OF 293-695 FROM N.A.
 RC TISSUE=Ovarian carcinoma;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Magatsuna M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Niimiya K., Iwayanagi T.;
 RT "NEO human cDNA sequencing project.";
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Possible adhesion molecule with a role in early
 CC hematopoiesis by mediating attachment to stromal cells. Influences
 CC the survival and/or proliferation of B cell precursors. Binding to
 CC cells requires Mn(II) (By similarity).
 CC -1- SUBUNIT: Oligomer with STM1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell surface
 CC (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed in all tissues and tumor cell lines
 CC examined.
 CC -1- PTM: Glycosylated.
 CC -1- PTM: Phosphorylated predominantly on Ser residues.
 CC -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
 CC
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 CC
 CC EMBL: AF328905; AAK82337.1; -;
 DR EMBL: AB040915; BAAG6006.1; ALT.INT.
 DR EMBL: AK033677; CAB66512.1; ALT.INT.
 DR EMBL: AK033693; BAB14545.1; ALT.SEO.
 DR InterPro: IPR001660; SAM.
 DR SMART: SM00454; SAM; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 KM Cell adhesion; Transmembrane; Coiled coil; Signal; Glycoprotein;
 KW Phosphorylation.
 FT SIGNAL 1 14
 FT CHAIN 15 746 STROMAL INTERACTION MOLECULE 2.

FT DOMAIN 15 217 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 218 235 POTENTIAL.
 FT DOMAIN 236 246 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 236 246 SAM.
 FT DOMAIN 242 344 COILED COIL (POTENTIAL).
 FT DOMAIN 358 394 COILED COIL (POTENTIAL).
 FT DOMAIN 533 559 HIS/PRO-RICH.
 FT DOMAIN 730 746 LYS-RICH.
 FT CARBOHYD 135 135 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 9 9 A -> P (IN REF. 3).
 FT CONFLICT 588 588 W -> WNTKCAAGDSQGFHVHGVAFDDFGSYSEKHK
 FT SEQUENCE 746 AA; 83971 MW; B8385557F126254 CRC64;
 SO
 Query Match 53.8%; Score 42; DB 1; Length 746;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 OY 1 AGESEPALYEDP 12
 DB 41 AAGDSPALMTDP 52
 PRT; 1149 AA.
 RESULT 8
 NOS2_CAVPO STANDARD; PRT; 1149 AA.
 ID NOS2_CAVPO
 AC 054705;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 DE (Inducible NOS) (INOS).
 GN NOS2 OR NOS.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley; TISSUE=Lung;
 RX MEDLINE=98343971; PubMed=9677342;
 RA Shirato M., Sakamoto T., Uchida Y., Nomura A., Ishii Y., Iijima H.,
 RA Goto Y., Hasegawa S.;
 RT "Molecular cloning and characterization of Ca2+-dependent inducible
 RT nitric oxide synthase from guinea-pig lung.";
 RL Biochem. J. 333:795-799(1998).
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
 CC -1- CATALYTIC ACTIVITY: L-arginine + NADPH + M O(2) = citrulline +
 CC nitric oxide + N NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF PAD AND FMN. ALSO REQUIRES
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
 CC THE ENZYME (BY SIMILARITY).
 CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
 CC WITH MOUSE NOS2).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LUNG AND COLON. NOT DETECTED
 CC IN THE HEART, AORTA, LIVER, KIDNEY, AND SPLEEN.
 CC -1- INDUCTION: BY LIPOPOLYSACCHARIDE (LPS); IN KIDNEY, SPLEEN, AND
 CC COLON. EXPRESSION IS REDUCED IN THE PRESENCE OF LPS IN LUNG.
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF027180; AAC3177.1; -;
 DR HSSP: P29477; 1DD7.
 DR InterPro: IPR003097; FAD_binding.

DR InterPro: IPR001709; FPN_cyl_redctase.
 DR InterPro: IPR001094; Flavodoxin_Like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR004030; NO_synthase.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR Pfam: PF00175; NAD_binding_1.
 DR Pfam: PF00258; Flavodoxin_1.
 DR Pfam: PF00667; FAD_binding_1.
 DR Pfam: PF02898; NO_synthase_1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 DR PROSITE: PS60001; NOS_1.
 KM Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
 KW Heme; Multigene family.
 FT BINDING 199 199 HEME (BY SIMILARITY).
 FT DOMAIN 308 328 CALMODULIN-BINDING (POTENTIAL).
 FT NP_BIND 622 653 FMN (PYRIMIDINE PART) (BY SIMILARITY).
 FT NP_BIND 766 777 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 902 912 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 977 995 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 1075 1090 NADP (ADP PART) (BY SIMILARITY).
 SQ SEQUENCE 1149 AA; 130631 MW; 60D595A2486DB50E CRC64;

Query Match 53.8%; Score 42; DB 1; Length 1149;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AGCGPALYEDPPD 14
 DB 310 ADGRDELFEIRPD 323

RESULT 9
 NS2A_HUMAN STANDARD; PRT; 1153 AA.
 ID NS2A_HUMAN
 AC P35228; Q16692; O60757; Q16263; O94994;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 DE (Inducible NOS) (iNOS) (Hepatocyte NOS) (HEP-NOS).
 GN NOS2A OR NOS2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-93234523; PubMed-7682706;
 RA Geller D.A., Lowenstein C.J., Shapiro R.A., Nussler A.K.,
 RA di Silvio M., Wang S.C., Nakayama D.K., Simmons R.L., Snyder S.H.,
 RA Billiar T.R.;
 RT "Molecular cloning and expression of inducible nitric oxide synthase
 from human hepatocytes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3491-3495(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Colorectal adenocarcinoma;
 RX MEDLINE-9403282; PubMed-7692964;
 RA Sherman P.A., Laubach V.E., Reep B.R., Wood E.R.;
 RT "Purification and cDNA sequence of an inducible nitric oxide synthase
 from a human tumor cell line.";
 RL Biochemistry 32:11600-11605(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Chondrocytes;
 RX MEDLINE-94068614; PubMed-7504305;
 RA Charles I.G., Palmer R.M.J., Hickery M.S., Bayliss M.T.,
 RA Chubb A.P., Hall V.S., Moss D.W., Moncada S.;
 RT "Cloning, characterization, and expression of a cDNA encoding an
 inducible nitric oxide synthase from the human chondrocyte.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11419-11423(1993).

RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Articular chondrocytes;
 RX MEDLINE-94368616; PubMed-7522054;
 RA Maier R., Bilbe G., Rediske J., Lotz M.;
 RT "Inducible nitric oxide synthase from human articular chondrocytes:
 RT cDNA cloning and analysis of mRNA expression.";
 RL Biochim. Biophys. Acta 1208:145-150(1994).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Retina;
 RX MEDLINE-95091827; PubMed-7528017;
 RA Park C.S., Pardhasaradhi K., Gianotti C., Villegas E., Krishna G.;
 RT "Human retina expresses both constitutive and inducible isoforms of
 RT nitric oxide synthase mRNA.";
 RL Biochem. Biophys. Res. Commun. 205:85-91(1994).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Glioblastoma;
 RX MEDLINE-95155267; PubMed-7531687;
 RA Hokari A., Zeniya M., Esumi H.;
 RT "Cloning and functional expression of human inducible nitric oxide
 RT synthase (NOS) cDNA from a glioblastoma cell line A-172.";
 RL J. Biochem. 116:575-581(1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Airway epithelium;
 RX MEDLINE-95372368; PubMed-7544004;
 RA Guo F.H., de Raeye R.H., Rice T.W., Stuehr D.J., Thunnissen F.B.J.M.,
 RA Erzurum S.C.;
 RT "Continuous nitric oxide synthase by inducible nitric oxide synthase
 RT in normal human airway epithelium in vivo.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7809-7813(1995).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Cardiac myocytes;
 RX MEDLINE-97304504; PubMed-9160867;
 RA Luss H., Li R.-K., Shapiro R.A., Zheng E., McGowan F.X., Yoneyama T.,
 RA Nakayama K., Geller D.A., Michle D.A.G., Simmons R.L.,
 RA Billiar T.R.;
 RT "Differentiated human ventricular cardiac myocytes express
 RT inducible nitric oxide synthase mRNA but not protein in response to
 RT IL-1, TNF, IFN-gamma, and LPS.";
 RL J. Mol. Cell. Cardiol. 29:1153-1165(1997).
 RN [9]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Ogawa Y., Nishijima S., Goto M., Ida M.;
 RT "Cloning and characterization of a novel splice variant of human
 RT inducible nitric oxide synthase.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE OF 380-473 FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE-95165725; PubMed-7532248;
 RA McIay J.S., Chatterjee P., Nicolson A.G., Jardine A.G., McKay N.G.,
 RA Ralston S.H., Grabowski P., Haines N.E., MacLeod A.M.,
 RA Hawksworth G.M.;
 RT "Nitric oxide production by human proximal tubular cells: a novel
 RT immunomodulatory mechanism?";
 RL Kidney Int. 46:1043-1049(1994).
 RN [11]
 RP CHARACTERIZATION.
 RX MEDLINE-96047340; PubMed-7558036;
 RA Bloch K.D., Wolfgram J.R., Brown D.M., Roberts J.D., Zapol D.G.,
 RA Lepore J.J., Filippov G., Thomas J.E., Jacob H.J., Bloch D.B.;
 RT "Three members of the nitric oxide synthase II gene family (NOS2a,
 RT NOS2b, and NOS2c) colocalize to human chromosome 17.";
 RL Genomics 27:526-530(1995).
 RN [12]
 RP CHARACTERIZATION.
 RX MEDLINE-98389865; PubMed-9721329;
 RA Taylor B.S., Alarcon L.H., Billiar T.R.;
 RT "Inducible nitric oxide synthase in the liver: regulation and

RT function.",
 RL Biochimica 63:766-781(1998).
 RM [13]
 RP X-RAY CRYSTALLOGRAPHY (2.55 ANGSTROMS) OF 74-504.
 RX MEDLINE-99340067; PubMed-10409685.
 RA Li H., Raman C.S., Glaser C.B., Blasco E., Young T.A., Parkinson J.F.,
 RA Whitlow M., Foulos T.L.,
 RA "Crystal structures of zinc-free and -bound heme domain of human
 RT inducible nitric-oxide synthase. Implications for dimer stability and
 RT comparison with endothelial nitric-oxide synthase.";
 RL J. Biol. Chem. 274:21276-21284(1999).
 RM [14]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 82-528.
 RX MEDLINE-99173237; PubMed-10074942;
 RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
 RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
 RA Weber P.C.;
 RT "Structural characterization of nitric oxide synthase isoforms
 RT reveals striking active-site conservation.";
 RL Nat. Struct. Biol. 6:233-242(1999).
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
 CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
 CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
 CC nitric oxide + N NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
 CC TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
 CC THE ENZYME (BY SIMILARITY).
 CC -1- ENZYME REGULATION: REGULATED BY CALCIUM/CALMODULIN (IN CONTRAST
 CC WITH MOUSE NOS2). ASPIRIN INHIBITS EXPRESSION AND FUNCTION OF THIS
 CC ENZYME AND EFFECTS MAY BE EXERTED AT THE LEVEL OF
 CC TRANSCRIPTIONAL/POSTTRANSCRIPTIONAL MODIFICATION AND DIRECTLY ON THE
 CC CATALYTIC ACTIVITY (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE LIVER, RETINA, BONE CELLS AND
 CC AIRWAY EPITHELIAL CELLS OF THE LUNG. NOT EXPRESSED IN THE
 CC PLATELETS.
 CC -1- INDUCTION: BY ENDOTOXINS AND CYTOKINES.
 CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.
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 CC -----
 DR EMBL: L09210; AAA59171.1; -;
 DR EMBL: L24553; AAA36375.1; -;
 DR EMBL: X73029; CAAS1512.1; -;
 DR EMBL: U05810; AAA56666.1; -;
 DR EMBL: U31511; AAB49041.1; -;
 DR EMBL: D26525; BAA05531.1; -;
 DR EMBL: U20141; AAB60366.1; -;
 DR EMBL: AF068236; AAC19133.1; -;
 DR EMBL: AB022318; BAA37123.1; -;
 DR EMBL: S75615; AAD14179.1; -;
 DR PIR: AA7475; A47475.
 DR PDB: INSI: 07-JAN-00.
 DR PDB: ZNSI: 07-JAN-00.
 DR PDB: ANOS: 04-FEB-00.
 DR GeneW: HGNC:7873; NOS2A.
 DR MIM: 163730; -;
 DR InterPro: IPR003097; FAD_binding.
 DR InterPro: IPR001709; FPN_cyl_redcse.
 DR InterPro: IPR001094; Flavodoxin_like.
 DR InterPro: IPR001226; Flavodoxin.
 DR InterPro: IPR004030; NO_synthase.
 DR InterPro: IPR001433; Oxred_FAD/NAO(P).
 DR Pfam: PF00175; NAD_binding; 1.

DR Pfam: PF00258; flavodoxin; 1.
 DR Pfam: PF00667; FAD_binding; 1.
 DR Pfam: PF02898; NO_synthase; 1.
 DR PRINTS: PR00369; FLAVODOXIN.
 DR PRINTS: PR00371; FPNCR.
 DR PROSITE: PS60001; NOS; 1.
 KW Oxidoreductase; NADP; FAD; FMN; Calcium-binding; Calmodulin-binding;
 KW Heme; Phosphorylation; Zinc; Metal-binding; Multigene family;
 KM Alternative splicing; 3D-structure.
 FT BINDING 200
 FT DOMAIN 509 529
 FT NP_BIND 623 654
 FT NP_BIND 767 778
 FT NP_BIND 903 913
 FT NP_BIND 978 996
 Query Match 53.8%; Score 42; DB 1; Length 1153;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 AGESEPALYEDPP 14
 Db 311 ANGRDPELEIIPP 324
 HAIR_RAT
 ID HAIR_RAT STANDARD; PRT; 1181 AA.
 AC P97609;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Hairless protein.
 GN HR.
 OS Rattus norvegicus (rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley;
 RX MEDLINE-97141510; PubMed-8987811;
 RA Thompson C.C.;
 RT "Thyroid hormone-responsive genes in developing cerebellum include a
 RT novel synaptotagmin and a hairless homolog.";
 RL J. Neurosci. 16:7832-7840(1996).
 CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
 CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -----
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 CC -----
 DR EMBL: U71293; AAC53018.1; ALT_INIT.
 DR InterPro: IPR003347; TF_JmJC.
 DR Pfam: PF02373; JmJC; 1.
 KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 KW Metal-binding.
 FT ZN_FING 594 619
 FT SEQUENCE 1181 AA; 127307 MW; 834B7029CF8E80F0 CRC64;
 SO
 Query Match 53.8%; Score 42; DB 1; Length 1181;
 Best Local Similarity 63.6%; Pred. No. 35;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 3 GEGPALYEDPP 13
 Db 578 GCGPATYEDSP 588

```

RESULT 11
HAIR_MOUSE
ID HAIR_MOUSE STANDARD: PRT: 1182 AA.
AC 061645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hairless protein.
GN HR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Skin;
RX MEDLINE-94329587; PubMed-8052649;
RA Cachon-Gonzalez M.B., Fennel S., Coffin J.M., Moran C., Best S.,
RA Stoye J.P.;
RT "Structure and expression of the hairless gene of mice.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR
CC FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN
CC DERMIS.
CC -1- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMozyGous FOR
CC SKIN TUMORS.
CC -----
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CC -----
DR EMBL: Z32675; CAAB3587.1; -.
DR MGD: MGI:96223; hr.
DR InterPro: IPR003347; TF_JmjC.
DR Pfam: PF02373; JmjC; 1.
KM Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
KM Metal-binding.
FT ZN_FING 595 620 CG-TYPE.
FT DOMAIN 535 540 POLY-GLY.
SQ SEQUENCE 1182 AA; 127182 MW; EFBBOEE62AE81B40 CRC64;

Query Match 53.8%; Score 42; DB 1; Length 1182;
Best Local Similarity 63.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 GEGPALYEDPP 13
ID 1:111:111
Db 579 GCGPAMTEDSP 589

RESULT 12
EXR3_ARATH
ID EXR3_ARATH STANDARD: PRT: 130 AA.
AC 092V52;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Expansin-related protein 3 precursor (Ath-ExpGamma-1.2).
DE

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GN EXR3 OR AT2G18660 OR MSF3.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Columbia;
RX MEDLINE-20083487; PubMed-10617197;
RA Lin X., Kaul S., Rounsley S.D., Shew T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGEC).";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE EXPANSIN FAMILY.
CC -1- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CC -----
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CC -----
DR EMBL: AC005724; M408935.1; ALT_INT.
DR EMBL: AT065269; M4138745.1; -.
DR PROSITE: PS50842; EXPANSIN_EG45; 1.
KM Glycoprotein; Signal; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 130 EXPANSIN-RELATED PROTEIN 3.
FT DOMAIN 28 130 EXPANSIN-LIKE EG45.
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 130 130 MISSING (IN REF. 1).
SQ SEQUENCE 130 AA; 14518 MW; BOC51C605043BC9 CRC64;

Query Match 52.6%; Score 41; DB 1; Length 130;
Best Local Similarity 58.3%; Pred. No. 4;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 AGECPALYEDPP 13
ID 1:111:111
Db 25 AAGCAVYVDPP 36

RESULT 13
NOS2_MOUSE
ID NOS2_MOUSE STANDARD: PRT: 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN NOS2 OR INOSL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-92229444; PubMed-1373522;
RA Xie Q.-W., Cho H.-J., Calaycay J., Munford R.A., Swiderek K.M.,
RA Lee T.D., Ding A., Troso T., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages.";
RN Science 256:225-228(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-92357701; PubMed-1379716;
RA Lowenstein C.J., Glat C.S., Bredt D.S., Snyder S.H.;
RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-92210618; PubMed-1372907;
RA Lyons C.R., Orloff G.J., Cunningham J.M.;
RT "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line.";
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-96088781; PubMed-7503239;
RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RT "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an MRL cell line.";
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=DA/2J, BALB/CBY, SJL/J, NOD/LTJ, and B10.S/J; TISSUE=Spleen;
RA Ma R.Z., Teuscher C.;
RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
RX MEDLINE-97477482; PubMed-9334294;
RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
RA Stuehr D.J., Tainer J.A.;
RT "The structure of nitric oxide synthase oxygenase domain and
RT inhibitor complexes.";
RL Science 278:425-431(1997).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
RX MEDLINE-20031637; PubMed-10562538;
RA Ghosh D.K., Crane B.R., Ghosh S., Nolan D., Gachhui R., Crooks C.,
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
RT hook and pterin-binding segment in dimerization and
RT tetrahydrobiopterin interaction.";
RL EMBO J. 18:6260-6270(1999).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
RX MEDLINE-98182450; PubMed-9516116;
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
RT substrate.";
RL Science 279:2121-2126(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
RX MEDLINE-20031638; PubMed-10562539;
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
RT "N-terminal domain swapping and metal ion binding in nitric oxide
RT synthase dimerization.";
RL EMBO J. 18:6271-6281(1999).
RN [10]
RP X-RAY CRYSTALLOGRAPHY OF (2.35 ANGSTROMS) 77-496.
RX MEDLINE-20233702; PubMed-10769116;
RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
RT nitric oxide synthase oxygenase dimer with active and inactive

RT pterins.";
RL Biochemistry 39:4608-4621(2000).
RN [11]
RP EFFECT OF ASPIRIN.
RC TISSUE-Macrophage;
RX MEDLINE-95372392; PubMed-7544010;
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
RA Weissmann G., Abramson S.B.;
RT "The mode of action of aspirin-like drugs: effect on inducible nitric
RT oxide synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
CC -I- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
CC WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY. IN MACROPHAGES, NO
CC MEDIATES TUMORICIDAL AND BACTERICIDAL ACTIONS.
CC -I- CATALYTIC ACTIVITY: L-arginine + NADPH + M O(2) -> citrulline +
CC nitric oxide + N NADP(+).
CC -I- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
CC TETRAHYDROBIOPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
CC THE ENZYME.
CC -I- ENZYME REGULATION: NOT STIMULATED BY CALCIUM/CALMODULIN. ASPIRIN
CC INHIBITS EXPRESSION AND FUNCTION OF THIS ENZYME AND EFFECTS MAY BE
CC EXERTED AT THE LEVEL OF TRANSLATIONAL/POSTTRANSLATIONAL
CC MODIFICATION AND DIRECTLY ON THE CATALYTIC ACTIVITY.
CC -I- SUBUNIT: HOMODIMER.
CC -I- TISSUE SPECIFICITY: MACROPHAGES.
CC -I- INDUCTION: BY TREATMENT WITH ENDOTOXINS OR CYTOKINES.
CC -I- SIMILARITY: BELONGS TO THE NOS FAMILY.
CC -----
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CC -----
CC EMBL; M87039; AAA39315.1; -;
CC EMBL; M92649; -; NOT_ANNOTATED_CDS.
CC EMBL; M84373; AAA39834.1; -;
CC EMBL; U43428; AAC52356.1; -;
CC EMBL; AF065919; AAC17914.1; -;
CC EMBL; AF065920; AAC17915.1; -;
CC EMBL; AF065921; AAC17916.2; -;
CC EMBL; AF065922; AAC17917.2; -;
CC EMBL; AF065923; AAC17918.2; -;
CC PIR; A43271; A43271.
CC PIR; A42166; A42166.
CC PDB; 1NOC; 18-NOV-98.
CC PDB; 1NOS; 18-NOV-98.
CC PDB; 2NOS; 18-NOV-98.
CC PDB; 1NOD; 23-MAR-99.
CC PDB; 2NOD; 23-MAR-99.
CC PDB; 3NOD; 23-MAR-99.
CC PDB; 1DF1; 08-DEC-99.
CC PDB; 1DMV; 04-FEB-00.
CC PDB; 1DMW; 06-FEB-00.
CC PDB; 1DMX; 06-FEB-00.
CC PDB; 1DOW; 15-DEC-99.
CC PDB; 1DD7; 29-MAR-00.
CC MGD; MGI:97361; Nos2.
CC InterPro: IPR003097; FAD_binding.
CC InterPro: IPR001709; FPN_cyt_redcse.
CC InterPro: IPR001094; Flavodoxin_like.
CC InterPro: IPR001226; Flavodoxin.
CC InterPro: IPR004030; NO_synthase.
CC InterPro: PF00175; NAD_binding_1.
CC Pfam: PF00258; Flavodoxin; 1.
CC Pfam: PF00667; FAD_binding; 1.
CC Pfam: PF02898; NO_synthase; 1.
CC PRINTS; PR00369; FLAVODOXIN.
CC PRINTS; PR00371; FPNCR.
CC PROSITE; PS60001; NOS; 1.

KM Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme;
 KM Zinc; Metal-binding; Multigene family; 3D-structure.
 FT BINDING 194 194 HEME.
 FT DOMAIN 503 523 CALMODULIN-BINDING (POTENTIAL).
 FT NP_BIND 617 648 FMN (PYRIDINE PART) (BY SIMILARITY).
 FT NP_BIND 761 772 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 897 907 FAD (FLAVIN PART) (BY SIMILARITY).
 FT NP_BIND 972 990 NADP (RIBOSE PART) (BY SIMILARITY).
 FT NP_BIND 1070 1085 NADP (ADP PART) (BY SIMILARITY).
 FT METAL 104 104 ZINC.
 FT METAL 109 109 ZINC.
 FT VARIANT 211 211 C -> R (IN STRAIN NOD/LTU).
 FT VARIANT 967 967 P -> L (IN STRAIN SJL/J).
 FT VARIANT 968 968 S -> F (IN STRAIN BALB/CBYJ).
 FT CONFLICT 19 19 K -> T (IN REF. 4).
 FT CONFLICT 191 191 A -> V (IN REF. 2).
 FT CONFLICT 844 844 A -> G (IN REF. 2).
 SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;
 Query Match 52.6%; Score 41; DB 1; Length 1144;
 Best Local Similarity 50.0%; Pred. No. 50;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 OY 1 AAGEGALYEDPPD 14
 DB 305 ADCQPEVEFEIPD 318
 RESULT 14
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 ID NOS2.RAT STANDARD; PRT; 1147 AA.
 AC 006518; P97774; 035765; 035765; 064558; 064005; 063267;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 GN (Inducible NOS) (INOS).
 OS NOS2.
 OC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Vascular smooth muscle;
 RX MEDLINE-93191721; PubMed7680561;
 RA Nunokawa Y., Ishida N., Tanaka S.;
 RT "Cloning of inducible nitric oxide synthase in rat vascular smooth
 muscle cells.";
 RL Biochem. Biophys. Res. Commun. 191:89-94(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mistar; TISSUE-Pancreatic islets;
 RX MEDLINE-95309542; PubMed7540573;
 RA Kariester A.E., Andersen H.U., Vissing H., Larsen P.M., Fey S.J.,
 RA Cuartero B.G., Madsen O.D., Petersen J.S., Mortensen S.B.,
 RA Mandrup-Poulsen T., Boel E., Nerup J.;
 RT "Cloning and expression of cytokine-inducible nitric oxide synthase
 cDNA from rat islets of Langerhans.";
 RL Diabetes 44:753-758(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Astrocytes;
 RX MEDLINE-94231594; PubMed7513765;
 RA Gale E., Reis D.J., Feinstein D.L.;
 RT "Cloning and expression of inducible nitric oxide synthase from rat
 astrocytes.";
 RL J. Neurosci. Res. 37:406-414(1994).
 RN [4]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE-Liver;
 RX MEDLINE-94039059; PubMed7693462;
 RA Adachi H., Iida S., Oguchi S., Ohshima H., Suzuki H., Nagasaki K.,
 RA Kawasaki H., Sugimura T., Esumi H.;
 RT "Molecular cloning of a cDNA encoding an inducible
 calmodulin-dependent nitric-oxide synthase from rat liver and its
 expression in COS 1 cells.";
 RL Eur. J. Biochem. 217:37-43(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Hepatocytes;
 RX MEDLINE-93221515; PubMed7682072;
 RA Wood E.R., Berger H. Jr., Sherman P.A., Lapetina E.G.;
 RT "Hepatocytes and macrophages express an identical cytokine inducible
 nitric oxide synthase gene.";
 RL Biochem. Biophys. Res. Commun. 191:767-774(1993).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Aorta;
 RX MEDLINE-94325351; PubMed7519448;
 RA Geng Y.J., Almqvist M., Hansson G.K.;
 RT "cDNA cloning and expression of inducible nitric oxide synthase from
 rat vascular smooth muscle cells.";
 RL Biochim. Biophys. Acta 1218:421-424(1994).
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Kosuga K., Yui Y., Hattori R., Sase K., Ezawa H., Aoyama T.,
 RA Inoue R., Sasayama S.;
 RT "Cloning of an inducible nitric oxide synthase from rat
 polymorphonuclear neutrophils.";
 RL Endothelium 2:217-221(1994).
 RN [8]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97070590; PubMed8913516;
 RA Tsutsunishita Y., Kawai Y., Takahara H., Ono T., Miyoshi J.,
 RA Futaki S., Niwa M.;
 RT "Sequence analysis of inducible nitric oxide synthase in rat kidney,
 lung, and uterus.";
 RL Biol. Pharm. Bull. 19:1374-1376(1996).
 RN [9]
 RP SEQUENCE OF 426-788 FROM N.A.
 RC STRAIN-Dahl/Rapp salt sensitive strain; TISSUE-Vascular smooth muscle;
 RX MEDLINE-98195092; PubMed9535415;
 RA Chen P.Y., Gladish R.D., Sanders P.M.;
 RT "Vascular smooth muscle nitric oxide synthase anomalies in Dahl/Rapp
 salt-sensitive rats.";
 RL Hypertension 31:918-924(1998).
 RN [10]
 RP SEQUENCE OF 509-740 FROM N.A.
 RC STRAIN-Mistar; TISSUE-Renal glomerulus;
 RA Saura M., Zaragoza C., Martinez-Dalmau R., Perez-Sala D., Lamas S.;
 RT "Advances in the studies of NO synthesis regulation in mesangial
 cells.";
 RL Nephrologia 16:35-39(1996).
 RN [11]
 RP SEQUENCE OF 479-655 FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Renal glomerulus;
 RX MEDLINE-94276509; PubMed7516453;
 RA Morrissey J.J., McCracken R., Kaneto H., Vehaskari M., Montani D.,
 RA Klahr S.;
 RT "Location of an inducible nitric oxide synthase mRNA in the normal
 kidney.";
 RL Kidney Int. 45:998-1005(1994).
 RN [12]
 RP SEQUENCE OF 420-479 FROM N.A.
 RC TISSUE-Myocardium;
 RA Mitchell T., Balligand J.-L.;
 RT "Isolation and characterization of iNOS from rat cardiocytes.";
 CC Submitted (SEP-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS A MESSENGER MOLECULE
 WITH DIVERSE FUNCTIONS THROUGHOUT THE BODY.
 CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) -> citrulline +
 nitric oxide + N NADP(+).
 CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES
 TETRAHYDROBIPTERIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF
 THE ENZYME.

[illegible]

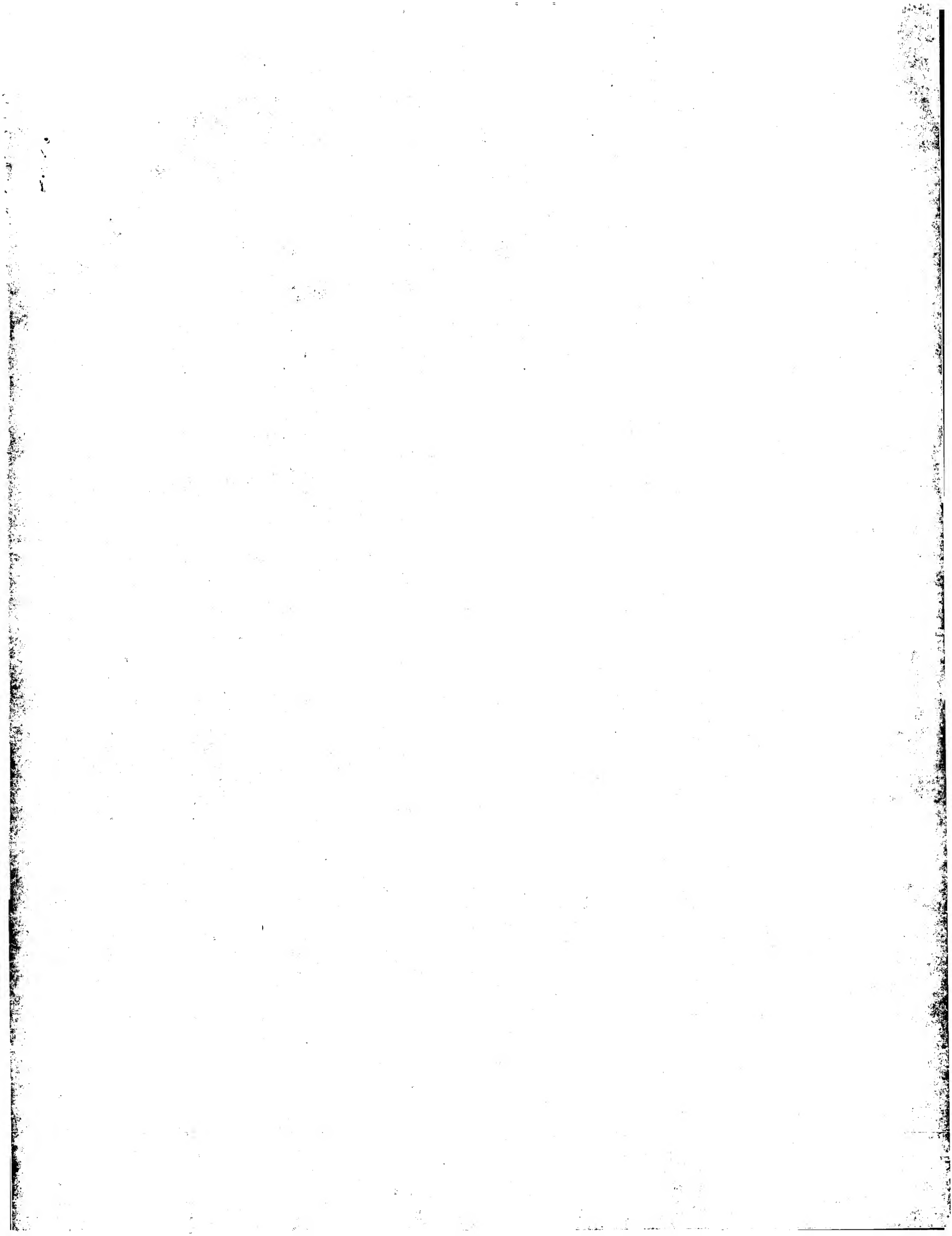
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DR InterPro: IPR001709; FPN_cyl_redcise.
DR InterPro: IPR001094; Flavodoxin_like.
DR InterPro: IPR001226; Flavodoxin.
DR InterPro: IPR004030; NO_synthase.
DR InterPro: IPR001433; Oxred_FAD/NAD(P).
DR Pfam: PF00175; NAD_binding_1.
DR Pfam: PF00258; Flavodoxin_1.
DR Pfam: PF00667; FAD_binding_1.
DR Pfam: PF02898; NO_synthase_1.
DR PRINTS: PR00369; FLAVODOXIN.
DR PRINTS: PR00371; FPNCR.
DR PROSITE: PS60001; NOS; 1.
DR Oxidoreductase: NADP: FAD: FMN: Calcium-binding; Calmodulin-binding;
KW Heme; Zinc; Metal-binding; Multigene family.
FT BINDING 197 197 HEME (BY SIMILARITY).
FT DOMAIN 506 526 CALMODULIN-BINDING (POTENTIAL).
FT NP_BIND 620 651 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 764 775 FAD (ADP PART) (BY SIMILARITY).
FT NP_BIND 900 910 FAD (FLAVIN PART) (BY SIMILARITY).
FT NP_BIND 975 993 NADP (RIBOSE PART) (BY SIMILARITY).
FT NP_BIND 1073 1088 NADP (ADP PART) (BY SIMILARITY).
FT METAL 107 107 ZINC (BY SIMILARITY).
FT METAL 112 112 ZINC (BY SIMILARITY).
FT CONFLICT 248 248 N -> S (IN REF. 1; AAC83554).
FT CONFLICT 271 271 D -> A (IN REF. 1; AAC83554).
FT CONFLICT 399 399 G -> E (IN REF. 1; AAC83554).
FT CONFLICT 640 640 P -> Q (IN REF. 1; AAC83554).
FT CONFLICT 731 731 A -> T (IN REF. 1; AAC83554).
FT CONFLICT 937 937 H -> N (IN REF. 1; AAC83554).
FT CONFLICT 1008 1009 TL -> NF (IN REF. 1; AAC83554).
FT CONFLICT 1024 1024 E -> K (IN REF. 1; AAC83554).
FT CONFLICT 1076 1076 I -> L (IN REF. 1; AAC83554).
FT CONFLICT 1129 1129 F -> V (IN REF. 1; AAC83554).
SQ SEQUENCE 1147 AA: 130528 MW: PF7E4C7ABA76D820 CRC64;

Query Match 52.6%; Score 41; DB 1; Length 1147;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 AAGEGPAlyEDPPD 14
DB 308 AHGODPEVEIIPP 321

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Search completed: January 30, 2003, 14:37:56
 Job time : 13 secs



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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:37:03 : Search time 14 Seconds
(without alignments)
29.423 Million cell updates/sec

Title: US-10-001-426-2
Perfect score: 78
Sequence: 1 AAGGSPALYEDPPD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/6CTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	78	100.0	318	2	US-08-872-719-2
3	78	100.0	318	3	US-08-957-302A-12
4	78	100.0	318	4	US-09-336-890-2
5	78	100.0	318	4	US-09-542-403-12
6	78	100.0	318	4	US-09-668-499-2
7	78	100.0	319	2	US-08-795-927-4
8	78	100.0	524	3	US-08-957-302A-2
9	78	100.0	524	4	US-09-542-403-2
10	78	100.0	1146	4	US-09-126-109-12
11	78	100.0	1153	1	US-08-314-917-2
12	78	100.0	1153	1	US-08-265-046-2
13	78	100.0	1153	1	US-08-465-522-2
14	78	100.0	1153	5	PCT-US93-11401-2
15	78	100.0	1153	5	PCT-US95-07849-2
16	78	100.0	1182	4	US-09-287-354-6
17	78	100.0	1207	4	US-09-287-354-5
18	78	100.0	1144	1	US-08-147-812-5
19	78	100.0	1144	2	US-08-319-866-12
20	78	100.0	1144	4	US-09-123-708-2
21	78	100.0	1144	4	US-09-123-624-2
22	78	100.0	1189	4	US-09-287-354-4
23	78	100.0	717	4	US-09-307-143-2
24	78	100.0	855	4	US-08-890-865A-10
25	78	100.0	933	4	US-08-764-870-14
26	78	100.0	933	4	US-08-980-115-14
27	78	100.0	1447	4	US-09-041-886-25

28	38	48.7	1447	5	PCT-US94-05277-2	Sequence 2, Appl1
29	37	47.4	86	2	US-08-343-443B-7	Sequence 7, Appl1
30	37	47.4	355	4	US-08-630-915A-192	Sequence 192, App
31	37	47.4	656	2	US-08-343-443B-2	Sequence 2, Appl1
32	37	47.4	656	4	US-09-214-564A-4	Sequence 4, Appl1
33	37	47.4	707	1	US-08-528-122-18	Sequence 18, Appl1
34	37	47.4	707	5	PCT-US95-11720-18	Sequence 62, Appl1
35	37	47.4	713	1	US-08-188-228-62	Sequence 56, Appl1
36	37	47.4	713	1	US-08-332-643-56	Sequence 62, Appl1
37	37	47.4	713	1	US-08-332-638-62	Sequence 62, Appl1
38	37	47.4	750	1	US-08-325-553-2	Sequence 2, Appl1
39	37	47.4	750	2	US-08-394-152A-2	Sequence 2, Appl1
40	37	47.4	750	4	US-09-044-668-2	Sequence 6, Appl1
41	37	47.4	1336	2	US-08-551-356-6	Sequence 6, Appl1
42	37	47.4	1336	5	PCT-US93-12687-6	Sequence 2, Appl1
43	37	47.4	2446	2	US-08-551-356-2	Sequence 2, Appl1
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45	36	46.2	71	4	US-09-188-930-338	

ALIGNMENTS

RESULT 1
US-08-795-927-2
Sequence 2, Application US/08795927
Patent No. 5986072
GENERAL INFORMATION:
APPLICANT: HANADA, Hiroshi
APPLICANT: KAWAGUCHI, Haruma
TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
TITLE OR INVENTION: PROCESS OF PURIFYING PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,927
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corleas, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-795-927-2

Query Match 100.0%; Score 78; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEYDDPPD 14
Db 1 AAGEGPALEYDDPPD 14

RESULT 2

US-08-872-719-2
Sequence 2, Application US/08872719

Patent No. 5919643

GENERAL INFORMATION:

APPLICANT: Kelley, Mark R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE USE OF APURINIC/APYRIMIDINIC

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77057-2198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/872,719

FILING DATE: CONCURRENTLY HEREWITH

CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: INDY:012P21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-872-719-2

Query Match 100.0%; Score 78; DB 2; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEYDDPPD 14

Db 37 AAGEGPALEYDDPPD 50

RESULT 3

US-08-957-302A-12

Sequence 12, Application US/08957302A

Patent No. 6046036

GENERAL INFORMATION:

APPLICANT: Kelley, Mark

APPLICANT: Williams, David

TITLE OF INVENTION: DNA Sequences Encoding Fusions of DNA

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TX

COUNTRY: US

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/957,302A

FILING DATE: CONCURRENTLY HEREWITH

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: INDY:005

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-957-302A-12

Query Match 100.0%; Score 78; DB 3; Length 318;

Best Local Similarity 100.0%; Pred. No. 2.7e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEYDDPPD 14

Db 37 AAGEGPALEYDDPPD 50

RESULT 4

US-09-336-890-2

Sequence 2, Application US/09336890

Patent No. 6190661

GENERAL INFORMATION:

APPLICANT: Kelley, Mark R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE USE OF

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DURKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TEXAS

COUNTRY: USA

ZIP: 77057-2198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/336, 890

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/872,719

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: INDY:012P21

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 318 amino acids

TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
US-09-336-890-2
Query Match          100.0%; Score 78; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPAlyEDPPD 14
Db 37 AAGEGPAlyEDPPD 50

RESULT 5
US-09-542-403-12
; Sequence 12, Application US/09542403
; Patent No. 6252048
; GENERAL INFORMATION:
; APPLICANT: Kelley, Mark
; ATTORNEY/AGENT INFORMATION:
; TITLE OF INVENTION: DNA Sequences Encoding Fusions of DNA
; TITLE OF INVENTION: Repair Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TX
; COUNTRY: US
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/542,403
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/957,302
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: INDY:005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-542-403-12
Query Match          100.0%; Score 78; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPAlyEDPPD 14
Db 37 AAGEGPAlyEDPPD 50

RESULT 6
US-09-668-499-2
; Sequence 2, Application US/09668499
; Patent No. 6406917
; GENERAL INFORMATION:
; APPLICANT: Kelley, Mark R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE USE OF APURINIC/ADYRIMIDINIC
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; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77057-2198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/668,499
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/872,719
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: INDY:012P21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-668-499-2
Query Match          100.0%; Score 78; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPAlyEDPPD 14
Db 37 AAGEGPAlyEDPPD 50

RESULT 7
US-08-795-927-4
; Sequence 4, Application US/08795927
; Patent No. 5986072
; GENERAL INFORMATION:
; APPLICANT: HANDA, HITOSHI
; ATTORNEY/AGENT INFORMATION:
; TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
; TITLE OF INVENTION: PROCESS OF PURIFYING PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,927
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
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ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-795-927-4

Query Match 100.0%; Score 78; DB 2; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
Db 37 AAGEGPALYEDPPD 50

RESULT 8

US-08-957-302A-2
Sequence 2, Application US/08957302A

GENERAL INFORMATION:
APPLICANT: Kelley, Mark
TITLE OF INVENTION: DNA Sequences Encoding Fusions of DNA
TITLE OF INVENTION: Repair Proteins and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,302A
FILING DATE: Concurrently Herewith
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INDY:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-957-302A-2

Query Match 100.0%; Score 78; DB 3; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGEGPALYEDPPD 14
Db 243 AAGEGPALYEDPPD 256

RESULT 9

US-09-542-403-2
Sequence 2, Application US/09542403

GENERAL INFORMATION:
APPLICANT: Kelley, Mark
TITLE OF INVENTION: DNA Sequences Encoding Fusions of DNA
TITLE OF INVENTION: Repair Proteins and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/542,403
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/957,302

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: INDY:005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 524 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-542-403-2

Query Match 100.0%; Score 78; DB 4; Length 524;
Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
Db 243 AAGEGPALYEDPPD 256

RESULT 10

US-09-126-109-12

Sequence 12, Application US/09126109
Patent No. 6171856

GENERAL INFORMATION:
APPLICANT: Thiipen, Anice
APPLICANT: Hohmeier, Hans-Ewald
APPLICANT: Newgard, Christopher B.
APPLICANT: Unger, Roger H.
APPLICANT: Shimabukuro, Michio
APPLICANT: Chen, Guaxun
APPLICANT: Rhodes, Christopher J.
APPLICANT: Hugl, Stigrun R.

APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
TO NO-MEDIATED CYTOTOXICITY
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,109
FILING DATE: 30-JUL-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,092
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US Unknown
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTS:560
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1146 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-126-109-12
Query Match 53.8%; Score 42; DB 4; Length 1146;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 1 AAGEGPAlyEDPPD 14
Db 311 ANGRDPELFETPPD 324
RESULT 11
US-08-314-917-2
Sequence 2, Application US/08314917
Patent No. 5468630
GENERAL INFORMATION:
APPLICANT: Billiar, Timothy R.
APPLICANT: Nussler, Andreas K.
APPLICANT: Geller, David A.
APPLICANT: Simmons, Richard L.
TITLE OF INVENTION: CDNA Clone for Human Inducible Nitric
Oxide Synthase And Process for Preparing Same
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold B. Silverman
STREET: Eckert Seamans Cherin & Melliott
CITY: Pittsburgh
STATE: PA
COUNTRY: USA
ZIP: 15219
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,917
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/981,344
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Silverman, Arnold B.
REGISTRATION NUMBER: 22,614
REFERENCE/DOCKET NUMBER: 116972
TELECOMMUNICATION INFORMATION:
TELEPHONE: (412) 566-6000
TELEFAX: (412) 566-6099
TELEX: 866172
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1153 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-314-917-2
Query Match 53.8%; Score 42; DB 1; Length 1153;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY 1 AAGEGPAlyEDPPD 14
Db 311 ANGRDPELFETPPD 324
RESULT 12
US-08-265-046-2
Sequence 2, Application US/08265046
Patent No. 5658565
GENERAL INFORMATION:
APPLICANT: Timothy R. Billiar
APPLICANT: Edith Tzeng
APPLICANT: Andreas K. Nussler
APPLICANT: David A. Geller
APPLICANT: Richard L. Simmons
TITLE OF INVENTION: Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lewis F. Gould, Jr.
STREET: Eckert Seamans Cherin & Melliott
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,046
FILING DATE: 24-JUN-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Lewis F. Jr.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 119130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6020
TELEFAX: (215) 575-6015
TELEX:

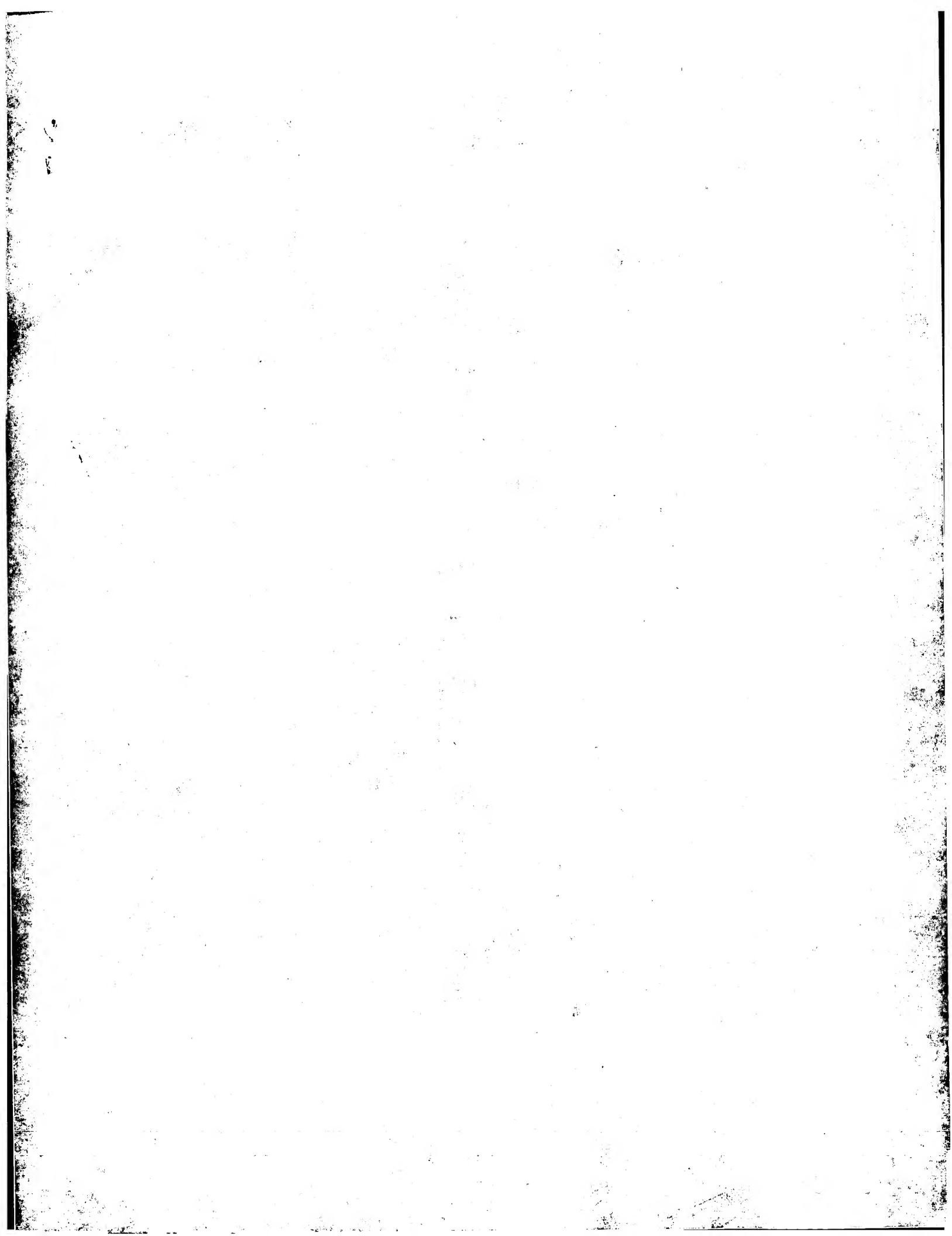

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/07849
: FILING DATE:
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: GOULD, Lewis F., Jr.
: REGISTRATION NUMBER: 25,057
: REFERENCE/DOCKET NUMBER: 119130-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 575-6020
: TELEFAX: (215) 575-6015
: TELEX:
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1153 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US95-07849-2

Query Match          53.8%; Score 42; DB 5; Length 1153;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGEGPALYEDPPD 14
   | | | | |
Db 311 ANGRDPELFELPPD 324
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Job time : 16 secs



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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:38:39 : Search time 10 Seconds
(without alignments)
28.250 Million cell updates/sec

Title: US-10-001-426-2

Sequence: 1 AAGEGALYEDPPD 14

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Post-processing: Minimum Match 0%
Maximum Match 100%
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- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	78	100.0	14	9	US-10-001-426-2
2	78	100.0	14	9	US-10-003-014-2
3	78	100.0	319	9	US-10-001-426-4
4	78	100.0	319	9	US-10-003-014-4
5	78	100.0	345	10	US-09-925-300-1188
6	44	56.4	68	10	US-09-925-297-551
7	42	53.8	1153	10	US-09-993-056-2
8	41	52.6	1144	9	US-09-870-759-124
9	39.5	50.6	561	9	US-09-822-364A-1
10	39.5	50.6	561	9	US-09-354-590-1
11	39.5	50.6	561	9	US-10-115-695-1
12	39	50.0	201	10	US-09-925-300-1432
13	39	50.0	563	9	US-09-738-626-6643
14	38	48.7	7968	9	US-10-077-130-5
15	38	48.7	114	10	US-09-994-365-3
16	38	48.7	136	10	US-09-994-365-2
17	38	48.7	456	10	US-09-815-242-10400
18	38	48.7	456	10	US-09-815-242-11073
19	38	48.7	456	10	US-09-815-242-14064

20	38	48.7	458	10	US-09-815-242-11759	Sequence 11759, A
21	37	47.4	15	9	US-09-942-117-14	Sequence 14, App11
22	37	47.4	91	9	US-09-942-117-4	Sequence 4, App11
23	37	47.4	171	10	US-09-925-301-1078	Sequence 1078, Ap
24	37	47.4	355	10	US-09-879-957-192	Sequence 192, App
25	37	47.4	368	10	US-09-925-299-888	Sequence 888, App
26	37	47.4	478	10	US-09-864-761-43251	Sequence 43251, A
27	37	47.4	448	10	US-09-939-521-7	Sequence 7, App11
28	37	47.4	733	10	US-09-862-027-42	Sequence 42, App1
29	37	47.4	750	9	US-09-978-295A-618	Sequence 618, App
30	37	47.4	750	9	US-09-978-697-618	Sequence 618, App
31	37	47.4	750	9	US-09-978-192A-618	Sequence 618, App
32	37	47.4	750	9	US-09-895-793-944	Sequence 944, App
33	37	47.4	750	9	US-09-999-832A-618	Sequence 618, App
34	37	47.4	750	9	US-09-978-189-618	Sequence 618, App
35	37	47.4	750	9	US-10-174-590-104	Sequence 104, App
36	37	47.4	750	9	US-10-175-758-104	Sequence 104, App
37	37	47.4	750	9	US-10-175-737-104	Sequence 104, App
38	37	47.4	750	10	US-09-823-827-944	Sequence 944, App
39	37	47.4	750	12	US-10-052-586-104	Sequence 104, App
40	37	47.4	3472	9	US-10-027-806-4	Sequence 4, App11
41	37	47.4	3472	9	US-10-034-623-4	Sequence 4, App11
42	36	46.2	71	9	US-09-981-876-239	Sequence 239, App
43	36	46.2	71	9	US-09-981-876-240	Sequence 240, App
44	36	46.2	88	10	US-09-864-761-42871	Sequence 42871, A
45	36	46.2	204	10	US-09-922-378-3	Sequence 3, App11

ALIGNMENTS

RESULT 1
US-10-001-426-2
; Sequence 2, Application US/10001426
; Patent No. US20020160472A1
; GENERAL INFORMATION:
; APPLICANT: HANDA, Hiroshi
; TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronsteijn, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/001,426
; FILING DATE: 02-NO. US20020160472A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/440,597
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corlees, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 47115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-001-426-2

Query Match 100.0%; Score 78; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEDPPD 14
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Db 1 AAGEGPALEDPPD 14

RESULT 2
US-10-003-014-2
; Sequence 2, Application US/10003014
; Patent No. US20020169293A1
; GENERAL INFORMATION:
; APPLICANT: HANDA, Hiroshi
; KAWAGUCHI, Haruma
; TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
; PROCESS OF PURIFYING PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,014
; FILING DATE: 02-No. US20020169293A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/440,597
; FILING DATE: 15-No. US20020169293A1-1999
; APPLICATION NUMBER: 08/795,927
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 47115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-003-014-2
Query Match 100.0%; Score 78; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGEGPALEDPPD 14
|||||
Db 1 AAGEGPALEDPPD 14

RESULT 3
US-10-001-426-4
; Sequence 4, Application US/10001426
; Patent No. US20020160472A1
; GENERAL INFORMATION:
; APPLICANT: HANDA, Hiroshi
; KAWAGUCHI, Haruma
; TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
; PROCESS OF PURIFYING PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/001,426
; FILING DATE: 02-No. US20020160472A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/440,597
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 47115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-001-426-4
Query Match 100.0%; Score 78; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGEGPALEDPPD 14
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Db 37 AAGEGPALEDPPD 50

RESULT 4
US-10-003-014-4
; Sequence 4, Application US/10003014
; Patent No. US20020169293A1
; GENERAL INFORMATION:
; APPLICANT: HANDA, Hiroshi

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; KAWAGUCHI, Haruma
; TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
; PROCESS OF PURIFYING PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, Bronsteijn, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,014
; FILING DATE: 02-NO. US20020169293A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/440,597
; FILING DATE: 15-NO. US20020169293A1-1999
; APPLICATION NUMBER: 08/795,937
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corleiss, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 47115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
; US-10-003-014-4
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Query Match          100.0%; Score 78; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 5.8e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAGEGPAlyEDPPD 14
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DB 37 AAGEGPAlyEDPPD 50
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RESULT 5
US-09-925-300-1188
; Sequence 1188, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 1188
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1188
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Query Match          100.0%; Score 78; DB 10; Length 345;
Best Local Similarity 100.0%; Pred. No. 6.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 64 AAGEGPAlyEDPPD 77
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RESULT 6
US-09-925-297-551
; Sequence 551, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 551
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (46)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-297-551
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Query Match          56.4%; Score 44; DB 10; Length 68;
Best Local Similarity 61.5%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 AAGEGPAlyEDPP 13
    |||:||||
DB 39 AAGEGPEXLEDPP 51
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RESULT 7
US-09-992-056-2
; Sequence 2, Application US/09992056
; Patent No. US20020061862A1
; GENERAL INFORMATION:
; APPLICANT: Ballier, Timothy R.
; APPLICANT: Tzenq, Edith
; APPLICANT: Nussler, Andreas K.
; APPLICANT: Geller, David A.
; APPLICANT: Simmons, Richard K.
; TITLE OF INVENTION: Inducible Nitric Oxide Synthase Gene for Treatment of
; FILE REFERENCE: 213298
; CURRENT APPLICATION NUMBER: US/09/992,056
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 09/176,496
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 08/465,522
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; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/314,917
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: 07/981,344
; PRIOR FILING DATE: 1992-11-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 1153
; TYPE: PRT
; ORGANISM: Induced Human Hepatocyte RNA
US-09-992-056-2

Query Match          53.8%; Score 42; DB 10; Length 1153;
Best Local Similarity 57.1%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAGEGPAIXEDPPD 14
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DB 311 ANGRDELEFEIPPD 324

RESULT 8
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match          52.6%; Score 41; DB 9; Length 1144;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 AAGEGPAIXEDPPD 14
   | | | | | | | | | |
DB 305 ADGODEPVEFEIPPD 318

RESULT 9
US-09-922-364A-1
; Sequence 1, Application US/09922364A
; Patent No. US20020155531A1
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,364A
; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-00073005
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 561 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
; NAME/KEY: protein
; LOCATION: 1..561
; OTHER INFORMATION: /note="human small conductance,
; calcium-activated potassium channel
; protein 1 (hSK1)"
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-922-364A-1

Query Match          50.6%; Score 39.5; DB 9; Length 561;
Best Local Similarity 69.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 3 GEGP-ALYEDPPD 14
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DB 33 GSGPGLGRDPPD 45

RESULT 10
US-09-254-590-1
; Sequence 1, Application US/09254590
; Patent No. US20020165379A1
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..561
OTHER INFORMATION: /note="human small conductance,
calcium-activated potassium channel
protein 1 (hsk1)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-254-590-1
Query Match 50.6%; Score 39.5; DB 9; Length 561;
Best Local Similarity 69.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
OY 3 GEGP-ALYEDPPD 14
Db 33 GSGPGALGRDPPD 45
RESULT 11
US-10-115-695-1
Sequence 1, Application US/10115695
Publication No. US20020192757A1
GENERAL INFORMATION:
APPLICANT: Adelman, John P.
Maylie, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/115,695
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FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..561
OTHER INFORMATION: /note="human small conductance,
calcium-activated potassium channel
protein 1 (hsk1)"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-115-695-1
Query Match 50.6%; Score 39.5; DB 9; Length 561;
Best Local Similarity 69.2%; Pred. No. 84;
Matches 9; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
OY 3 GEGP-ALYEDPPD 14
Db 33 GSGPGALGRDPPD 45
RESULT 12
US-09-925-300-1432
Sequence 1432, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1690
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1432
LENGTH: 201
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (114)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (193)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; NAME/KEY: SITE
; LOCATION: (201)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1432
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Query Match
Best Local Similarity 72.7%; Score 39; DB 10; Length 201;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 3 GEGPALYEDPP 13
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Db 70 GEGPALYEDPP 80
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RESULT 13
US-09-738-626-6643
; Sequence 6643, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, MAKOTO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6643
; LENGTH: 563
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6643
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Query Match
Best Local Similarity 50.0%; Score 39; DB 9; Length 563;
Matches 8; Conservative 2; Mismatches 1; Indels 4; Gaps 1;
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QY 3 GEGP---ALYEDPP 13
    | : | | | |
Db 319 GDGPRTIDALYEDTP 333
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```
RESULT 14
US-10-077-130-5
; Sequence 5, Application US/10077130
; Patent No. US2002018742A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MP12001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/10/077,130
; CURRENT FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
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; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-077-130-5
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Query Match
Best Local Similarity 50.0%; Score 39; DB 9; Length 7968;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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```
QY 1 AAGEGPALYEDPPD 14
    : | | | | | | |
Db 5034 SADEGPAPPEPPAD 5047
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RESULT 15
US-09-994-365-3
; Sequence 3, Application US/0994365
; Patent No. US20020115148A1
; GENERAL INFORMATION:
; APPLICANT: Charney, Patrick
; APPLICANT: Moss, Patrick
; APPLICANT: McEuen, Mark
; TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
; FILE REFERENCE: CECH18109
; CURRENT APPLICATION NUMBER: US/09/994,365
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/253,592
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/256,839
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-994-365-3
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Query Match
Best Local Similarity 48.7%; Score 38; DB 10; Length 114;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 6 PALYEDPP 13
    | : | | | |
Db 36 PPLFEDPP 43
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Search completed: January 30, 2003, 14:42:23
Job time : 11 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:37:44 : Search time 139 Seconds
(Without alignments)
64.937 Million cell updates/sec

Title: US-10-001-426-2

Perfect score: 78
Sequence: 1 AAGEGPALEDPPD 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

1:	/cgn2_6/ptodata/1/paa/PCRTUS.COMB.pep.*
2:	/cgn2_6/ptodata/1/paa/US07.COMB.pep.*
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5:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
6:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
7:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
8:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
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10:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
11:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
12:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
13:	/cgn2_6/ptodata/1/paa/US08.COMB.pep.*
14:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
15:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
16:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
17:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
18:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
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20:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
21:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
22:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
23:	/cgn2_6/ptodata/1/paa/US09.COMB.pep.*
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25:	/cgn2_6/ptodata/1/paa/US10.COMB.pep.*
26:	/cgn2_6/ptodata/1/paa/US10.COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US10.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	78	100.0	14	US-09-440-597-2
2	78	100.0	14	US-10-001-426-2
3	78	100.0	14	US-10-003-014-2
4	78	100.0	69	US-10-029-386-28638
5	78	100.0	73	US-09-834-366-16628
6	78	100.0	73	US-60-197-873-16628

7	78	100.0	146	US-09-791-537-41381
8	78	100.0	170	PCT-US01-18569-4083
9	78	100.0	170	US-10-264-049-4083
10	78	100.0	183	US-09-760-482-73
11	78	100.0	183	US-09-760-485-815
12	78	100.0	183	US-10-153-088-73
13	78	100.0	183	US-10-216-436-815
14	78	100.0	287	US-09-791-537-102207
15	78	100.0	285	US-09-805-020-48
16	78	100.0	300	PCT-US02-30474-1725
17	78	100.0	300	US-60-324-631-1730
18	78	100.0	317	US-09-791-537-125777
19	78	100.0	318	US-08-957-302-12
20	78	100.0	318	US-09-522-046-2
21	78	100.0	318	US-09-791-537-31856
22	78	100.0	318	US-09-791-537-61013
23	78	100.0	318	US-09-791-537-78158
24	78	100.0	318	US-09-791-537-79508
25	78	100.0	318	US-09-791-537-114574
26	78	100.0	318	US-09-976-594-938
27	78	100.0	318	US-10-247-671-132400
28	78	100.0	318	US-60-240-409-938
29	78	100.0	318	US-60-323-784-131
30	78	100.0	319	US-10-001-426-4
31	78	100.0	319	US-10-001-426-4
32	78	100.0	319	US-10-003-014-4
33	78	100.0	342	US-09-805-020-49
34	78	100.0	345	PCT-US00-05988-1188
35	78	100.0	345	US-09-925-300-1188
36	78	100.0	522	US-08-957-102-2
37	74	94.9	316	US-09-791-537-91767
38	74	94.9	317	US-09-791-537-8668
39	74	94.9	317	US-09-791-537-130991
40	64	82.1	219	US-09-791-537-67773
41	64	82.1	219	US-09-791-537-44105
42	62	79.5	318	US-09-791-537-114573
43	46	59.0	276	US-09-791-537-67718
44	46	59.0	577	US-09-802-540-12583
45	45	57.7	438	US-09-791-537-145174

ALIGNMENTS

RESULT 1
US-09-440-597-2
: sequence 2, Application US/09440597
: GENERAL INFORMATION:
: APPLICANT: KANAGUCHI, Haruma
: TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
: PROCESS OF PURIFYING PROTEINS
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/440,597
: FILING DATE: 15-Nov-1999
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/795,927
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:

NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-440-597-2

Query Match
Best Local Similarity 100.0%; Score 78; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14
Db 1 AAGEGPALYEDPPD 14

RESULT 2
US-10-001-426-2
Sequence 2, Application US/10001426
GENERAL INFORMATION:
APPLICANT: HANDA, Hiroshi
KAWAGUCHI, Haruma
TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
PROCESS OF PURIFYING PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/001,426
FILING DATE: 02-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/440,597
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-001-426-2

Query Match
Best Local Similarity 100.0%; Score 78; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14
Db 1 AAGEGPALYEDPPD 14

RESULT 3
US-10-003-014-2
Sequence 2, Application US/10003014
GENERAL INFORMATION:
APPLICANT: HANDA, Hiroshi
KAWAGUCHI, Haruma
TITLE OF INVENTION: DRUG-IMMOBILIZED PARTICLES AND A
PROCESS OF PURIFYING PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/003,014
FILING DATE: 02-Nov-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/440,597
FILING DATE: 15-Nov-1999
APPLICATION NUMBER: 08/795,927
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 47115
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-003-014-2

Query Match
Best Local Similarity 100.0%; Score 78; DB 24; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 1 AAGEGPAlyEDPPD 14
|||||

RESULT 4
US-10-029-386-28638

; Sequence 28638, Application US/10029386
; GENERAL INFORMATION:

; APPLICANT: Penn, Sharon G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G

; FILE REFERENCE: AEMICA-X-2

; CURRENT APPLICATION NUMBER: US/10/029,386

; CURRENT FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 34288

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 28638

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: MAP TO CHR14.1

; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1

; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.91

; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5

; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2

; OTHER INFORMATION: SWISSPROT HIT: p27695, EVALU = 3.00e-24

US-10-029-386-28638

Query Match 100.0%; Score 78; DB 24; Length 69;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPAlyEDPPD 14
|||||

Db 22 AAGEGPAlyEDPPD 35

RESULT 5

US-09-834-366-16628

; Sequence 16628, Application US/09834366
; GENERAL INFORMATION:

; APPLICANT: Benjamin, Stephane

; APPLICANT: Tanaka, Hiroaki

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Jobert, Severin

; APPLICANT: Giordano, Jean-Yves

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: 81.US2.REG

; CURRENT APPLICATION NUMBER: US/09/834,366

; CURRENT FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: US 60/197,873

; PRIOR FILING DATE: 2000-04-18

; NUMBER OF SEQ ID NOS: 52153

; SOFTWARE: Patent.pm

; SEQ ID NO 16628

; LENGTH: 73

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 59

; OTHER INFORMATION: Xaa = Pro,Thr

US-09-834-366-16628

Query Match 100.0%; Score 78; DB 22; Length 73;

Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPAlyEDPPD 14
|||||

Db 37 AAGEGPAlyEDPPD 50

RESULT 6
US-60-197-873-16628

; Sequence 16628, Application US/60197873
; GENERAL INFORMATION:

; APPLICANT: Benjamin, Stephane

; APPLICANT: Tanaka, Hiroaki

; APPLICANT: Dumas Milne Edwards, Jean Baptiste

; APPLICANT: Jobert, Severin

; APPLICANT: Giordano, Jean-Yves

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: 81.US1.PRO

; CURRENT APPLICATION NUMBER: US/60/197,873

; CURRENT FILING DATE: 2000-04-18

; NUMBER OF SEQ ID NOS: 52153

; SOFTWARE: Patent.pm

; SEQ ID NO 16628

; LENGTH: 73

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: 59

; OTHER INFORMATION: Xaa = Pro,Thr

US-60-197-873-16628

Query Match 100.0%; Score 78; DB 27; Length 73;

Best Local Similarity 100.0%; Pred. No. 0.00018;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPAlyEDPPD 14
|||||

Db 37 AAGEGPAlyEDPPD 50

RESULT 7
US-09-791-537-41381

; Sequence 41381, Application US/09791537
; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: Patent version 3.0

; SEQ ID NO 41381

; LENGTH: 146

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-41381

Query Match 100.0%; Score 78; DB 21; Length 146;

Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPAlyEDPPD 14
|||||

Db 37 AAGEGPAlyEDPPD 50

RESULT 8

PCT-US01-18569-4083

; Sequence 4083, Application PC/TUS0118569
; GENERAL INFORMATION:

US-09-834-366-16628

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; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA133PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4083
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (61)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-4083
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Query Match          100.0%; Score 78; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAGEGPALYEDPPD 14
Db 68 AAGEGPALYEDPPD 81
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```
RESULT 9
US-10-264-049-4083
; Sequence 4083, Application US/10264049
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133PCT
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4083
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (61)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4083
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Query Match          100.0%; Score 78; DB 26; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAGEGPALYEDPPD 14
Db 68 AAGEGPALYEDPPD 81
```

```
RESULT 10
US-09-760-482-73
; Sequence 73, Application US/09760482
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT260
; CURRENT APPLICATION NUMBER: US/09/760,482
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 215
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```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (182)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-482-73
```

```
Query Match          100.0%; Score 78; DB 21; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AAGEGPALYEDPPD 14
Db 64 AAGEGPALYEDPPD 77
```

```
RESULT 11
US-09-760-485-815
; Sequence 815, Application US/09760485
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ217
; CURRENT APPLICATION NUMBER: US/09/760,485
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 815
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (182)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-760-485-815
```

```
Query Match          100.0%; Score 78; DB 21; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 AAGEGPALYEDPPD 14
Db 64 AAGEGPALYEDPPD 77
```

```
RESULT 12
US-10-153-088-73
; Sequence 73, Application US/10153088
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT260CIN
; CURRENT APPLICATION NUMBER: US/10/153,088
; CURRENT FILING DATE: 2002-05-23
; Prior application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (182)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-153-088-73
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Query Match          100.0%; Score 78; DB 25; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AAGEGPALYEDPPD 14
DB 64 AAGEGPALYEDPPD 77
```

RESULT 13

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US-10-216-436-815
; Sequence 815, Application US/10216436
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P0217C1N
; CURRENT APPLICATION NUMBER: US/10/216,436
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 09/760,485
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1477
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 815
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (182)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-216-436-815
```

```
Query Match          100.0%; Score 78; DB 26; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AAGEGPALYEDPPD 14
DB 64 AAGEGPALYEDPPD 77
```

```
RESULT 14
US-09-791-537-102207
; Sequence 102207, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Dancer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 102207
; LENGTH: 287
; TYPE: PRT
; ORGANISM: pdb 1BIX
US-09-791-537-102207
```

```
Query Match          100.0%; Score 78; DB 21; Length 287;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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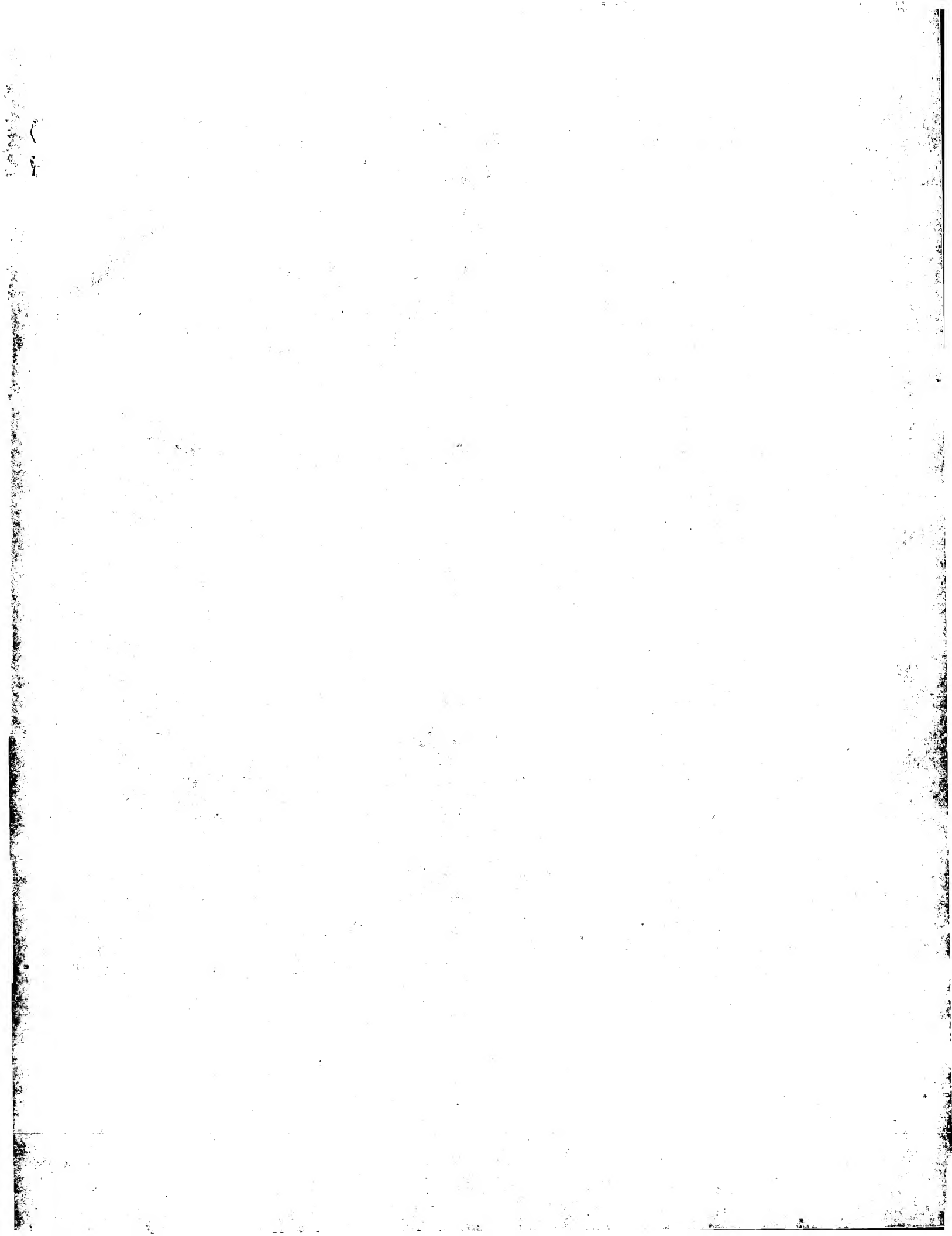
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OY 1 AAGEGPALYEDPPD 14
DB 6 AAGEGPALYEDPPD 19
```

```
RESULT 15
US-09-805-020-48
; Sequence 48, Application US/09805020
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurilt
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 48
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-020-48
```

```
Query Match          100.0%; Score 78; DB 22; Length 295;
Best Local Similarity 100.0%; Pred. No. 0.00092;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 AAGEGPALYEDPPD 14
DB 37 AAGEGPALYEDPPD 50
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Search completed: January 30, 2003, 14:41:41
Job time : 141 secs



Db 24 AAGEGPALYEDPPD 37

RESULT 3

```
US-09-724-676A-91737
; Sequence 91737, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91737
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91737
```

Query Match

100.0%; Score 78; DB 5; Length 282;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 24 AAGEGPALYEDPPD 37

RESULT 4

```
US-09-724-676A-91739
; Sequence 91739, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91739
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91739
```

Query Match

100.0%; Score 78; DB 5; Length 282;

Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 24 AAGEGPALYEDPPD 37

RESULT 5

```
US-09-724-676-91745
; Sequence 91745, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91745
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91745
```

Query Match

100.0%; Score 78; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 35 AAGEGPALYEDPPD 48

RESULT 6

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US-09-724-676-91746
; Sequence 91746, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91746
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91746
```

Query Match

100.0%; Score 78; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 35 AAGEGPALYEDPPD 48

RESULT 7

```
US-09-724-676-91758
; Sequence 91758, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91758
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91758
```

Query Match

100.0%; Score 78; DB 5; Length 293;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14

Db 35 AAGEGPALYEDPPD 48

RESULT 8

```
US-09-724-676-91759
; Sequence 91759, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91759
; LENGTH: 293
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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91759

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 9
US-09-724-676-91769
; Sequence 91769, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91769
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91769

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 10
US-09-724-676-91770
; Sequence 91770, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91770
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-91770

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 11
US-09-724-676A-91745
; Sequence 91745, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A

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; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91745
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91745

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 12
US-09-724-676A-91746
; Sequence 91746, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91746
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91746

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 13
US-09-724-676A-91758
; Sequence 91758, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91758
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91758

```

```

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 AAGEGPALEYDDPD 14
Db 35 AAGEGPALEYDDPD 48

```

```

RESULT 14
US-09-724-676A-91759
; Sequence 91759, Application US/09724676A

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; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91759
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91759

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
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Db 35 AAGEGPALYEDPPD 48

RESULT 15
US-09-724-676A-91769
; Sequence 91769, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91769
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-91769

Query Match
Best Local Similarity 100.0%; Score 78; DB 5; Length 293;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
   |||||||
Db 35 AAGEGPALYEDPPD 48
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Search completed: January 30, 2003, 14:42:05
Job time : 19 secs

Thu Jan 30 17:27:57 2003

us-10-001-426-2.rag

NEFF
10/001, 426

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:23:48 ; Search time 35 Seconds
(without alignments)
53.300 Million cell updates/sec

Title: US-10-001-426-2

Perfect score: 78
Sequence: 1 AAGECPALYEDPPD 14

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23:	/SID52/gcgdata/geneeq/geneeqp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	78	100.0	14	18	AAW21748	Fragment #2 of E33
2	78	100.0	170	23	ABP42951	Human ovarian anti
3	78	100.0	318	18	AAW21746	E3330-binding prot
4	78	100.0	318	19	AAW48894	Homo sapiens AP en
5	78	100.0	318	19	AAW52864	Apurinic/apyrimidi
6	78	100.0	345	21	AAW56610	Human prostate can
7	78	100.0	324	19	AAW48893	Homo sapiens MGMT-
8	45	57.7	364	22	AAW54366	Protonibacterium
9	44	56.4	68	21	AAW54099	Human pancreatic c
10	43	55.1	241	22	AAU47601	Protonibacterium

11	43	55.1	999	21	AAW53685
12	43	55.1	1008	21	AAW53684
13	43	55.1	1065	21	AAW53683
14	42	53.8	115	19	AAV21361
15	42	53.8	383	23	ABW97554
16	42	53.8	384	22	AAW67464
17	42	53.8	583	22	ABW71010
18	42	53.8	1017	22	AAW95217
19	42	53.8	1146	20	AAW96322
20	42	53.8	1153	15	AAW57664
21	42	53.8	1153	15	AAW63206
22	42	53.8	1153	17	AAW88464
23	42	53.8	1153	19	AAW36113
24	42	53.8	1153	22	AAW64497
25	42	53.8	1153	22	AAW64498
26	42	53.8	1153	22	AAW31724
27	42	53.8	1153	22	AAW66724
28	42	53.8	1153	22	AAW67463
29	42	53.8	1182	23	AAW19798
30	42	53.8	1207	23	AAW19797
31	41	52.6	107	22	AAW51428
32	41	52.6	314	22	AAW94555
33	41	52.6	1144	16	AAW77360
34	41	52.6	1144	19	AAW51246
35	41	52.6	1144	22	AAW64500
36	41	52.6	1147	17	AAW02571
37	41	52.6	1189	23	AAW19796
38	41	52.6	1319	22	ABG22751
39	40	51.3	65	22	AAU31478
40	40	51.3	100	22	AAU31479
41	40	51.3	134	21	AAW41036
42	40	51.3	134	23	AAW14447
43	40	51.3	491	22	AAW39422
44	40	51.3	825	15	AAW60811
45	40	51.3	904	22	ABG20852

ALIGNMENTS

RESULT 1
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ID AAW21748 standard; peptide: 14 AA.
AC AAW21748;
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DT 02-MAR-1998 (first entry)
XX
DE Fragment #2 of E3330-binding protein, Ref-1.
XX
KW E3330-binding protein; Ref-1; microsphere; drug binding factor recovery;
KW styrene-glycidyl methacrylate polymer; protein isolation;
KW protein purification; receptor identification.
XX
OS Synthetic.
XX
PN EP78988-A2.
XX
PD 06-AUG-1997.
XX
PF 05-FEB-1997; 97EP-0101821.
XX
PR 17-SEP-1996; 96JP-0266711.
PR 05-FEB-1996; 96JP-0018827.
PA (HAND/) HANDA H.
PA (KAWA/) KAWAGUCHI H.
XX
PI Handa H, Kawaguchi H;
XX
DR WPI; 1997-387634/36.
XX
PT Isolation and identification of receptors to specific compounds -

PT using microspheres prepared by coupling the compound, via a spacer, to a styrene-glycidyl methacrylate polymer.

PS Example 9; Page 10; 29pp; English

CC AAM2174W121749 represent fragments of the E3330-binding protein, Ref-1
CC (see AAM2174W121749). E3330 is
CC 3-(1-(5-(2,3-dimethoxy-6-methyl-1,4-benzoquinonyl))-2-nonyl-2-propionic
CC acid. Ref-1 was isolated using the method of the invention. The method
CC of the invention is for isolating a substance (S1) that can adhere to a
CC substance (S2) possessing physiological activity from a mixture
CC containing S1. The method comprises contacting the mixture with a
CC microsphere prepared by coupling S2 to a styrene-glycidyl methacrylate
CC polymer through a spacer. The process is useful, e.g., for recovery of
CC drug binding factors (such as proteins) from cell extracts. The process
CC allows easy isolation, purification and identification of receptors to
CC specific compounds.

SQ Sequence 14 AA;

Query Match	100.0%	Score 78;	DB 18;	Length 14;
Best Local Similarity	100.0%;	Pred. No.	1.1e-05;	
Matches 14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY 1 AAGEGPALYEDPPD 14
    |||||||
Db 1 AAGEGPALYEDPPD 14
```

Db 1 AAGGPPALYEDPPD 14

RESULT 2	
ABP42951	
ID	ABP42951 standard; Protein; 170 AA

AC ABP42951;

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HPDVI25, SEQ ID NO:4083.

KM Human ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KM ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KM infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KM PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KM inflammatory condition; immune disorder; blood disorder;
 KM gynaecological disorder; respiratory system disorder; neurological disorder;
 KM gastrointestinal disorder; urinary system disorder; drug screening;
 KM gene therapy; chromosome mapping; forensic analysis;
 KM antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KM antiinflammatory; gynaecological; reproductive.

OS Homo sapiens.

PN WO200200677-A1

PD 03-JAN-2002.

PF 07-JUN-2001; 2001WO-US18569.

PR 07-JUN-2000; 2000US-209467P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Blrse CE, Rosen CA;

DR WPI; 2002-147878/19.

XX

PT Isolated nucleic acid molecules encoding novel ovarian polypeptides
PT useful in the prevention, treatment and diagnosis of cancer (e.g.,
PT ovarian cancer), immune disorders, cardiovascular disorders and
PT neurological diseases -

PS Claim 11; SEQ ID No 4083; 2922pp; English.

XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 170 AA;

SQ Sequence 170 AA;

Query Match	100.0%	Score 78:	DB 23:	Length 170;
Best Local Similarity	100.0%;	Pred. No.	0.00014;	
Matches 14; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

```
QY      1 AAGEGPALYEDPPD 14
        |||
Db      68 AAGEGPALYEDPPD 81
```

Db 68 AAGEGPALYEDPPD 81

RESULT 3
AAW21746
ID AAW21746 standard; protein; 318 AA

AC AAW21746;

DT 02-MAR-1998 (first entry)

DE E3330-binding protein, Ref-1.

KM E3330-binding protein; Ref-1; microsphere; drug binding factor recovery;
KM styrene-glycidyl methacrylate polymer; protein isolation;
KM protein purification; receptor identification.

OS Synthetic.

PN EP787988-A2.

06-AUG-1997 PD

05-FEB-1997; 97EP-0101821.

PR 17-SEP-1996; 96JP-0266711.

XX	3	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
----	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

PA (KAWA/) KAWAGUCHI H.

PI Handa H, Kawaguchi H;

DR WPI; 1997-387634/36.

DR WPI; 1997-387634/36.

XX Isolation and identification of receptors to specific compounds -
PT using microspheres prepared by coupling the compound, via a spacer,
PT to a styrene-glycidyl methacrylate polymer.
XX
PS Claim 5; Page 11; 29pp; English.
XX
CC This sequence represents the E3330-binding protein, Ref-1. E3330 is
CC 3-[(5-(2,3-dimethoxy-6-methyl-1,4-benzoquinonyl)-2-nonyl-2-propionyl
CC acid. This sequence was isolated using the method of the invention. The
CC method of the invention is for isolating a substance (S1) that can adhere
CC to a substance (S2) possessing physiological activity from a mixture
CC containing S1. The method comprises contacting the mixture with a
CC microsphere prepared by coupling S2 to a styrene-glycidyl methacrylate
CC polymer through a spacer. The process is useful, e.g., for recovery of
CC drug binding factors (such as proteins) from cell extracts. The process
CC allows easy isolation, purification and identification of receptors to
CC specific compounds.
XX
SO Sequence 318 AA;
XX
Query Match 100.0%; Score 78; DB 18; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGEGPAlyEDPPD 14
DB 37 AAGEGPAlyEDPPD 50
XX
RESULT 4
AAW48894
ID AAW48894 standard; Protein; 318 AA.
XX
AC AAW48894;
XX
DT 13-OCT-1998 (first entry)
XX
DE Homo sapiens AP endonuclease.
XX
XX MGMT; APE; DNA repair protein; fusion protein; AP endonuclease;
KM 0-6-methylguanine-DNA methyltransferase.
XX
OS Homo sapiens.
XX
XX WO9817684-A2.
XX
XX 30-APR-1998.
XX
XX 24-OCT-1997; 97WO-US19629.
XX
XX 25-OCT-1996; 96US-0029308.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX Kelley M, Williams D;
XX
XX WPI: 1998-271785/24.
XX
XX N-PSDB: AAV32543.
XX
XX New fusion proteins comprising 2 DNA repair proteins - used for
PT protecting cells against DNA damage, e.g. by chemotherapeutic
PT agents, or for treating DNA-repair-defective human diseases
XX
XX Disclosure; p115-116; 150pp; English.
XX
CC The sequence is that encoding the APE gene which was used in the
CC construction of a fusion protein of the DNA repair
CC proteins 0-6-methylguanine-DNA methyltransferase (MGMT) and AP
CC endonuclease (APE). It can be used for protecting cells
CC (especially bone marrow cells) against DNA damaging agents such as
CC chemotherapeutic agents used in tumour therapy and can be used in
CC conjunction with chemotherapy to facilitate the use of increased doses

CC of chemotherapy. They can provide added protection to cells by
CC providing RPS which recognise different types of DNA lesions. In
CC addition, the RPS can be used in the treatment of DNA-repair-defective
CC human diseases, e.g. xeroderma pigmentosum, Ataxia telangiectasia,
CC Cockayne's syndrome, Bloom's syndrome, Fanconi's anemia, Parkinson's
CC disease and other neurodegenerative diseases including amyotrophic
CC lateral sclerosis, Alzheimer's disease and other age related disorders.
XX
SO Sequence 318 AA;
XX
Query Match 100.0%; Score 78; DB 19; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGEGPAlyEDPPD 14
DB 37 AAGEGPAlyEDPPD 50
XX
RESULT 5
AAW52864
ID AAW52864 standard; Protein; 318 AA.
XX
AC AAW52864;
XX
DT 08-JUL-1998 (first entry)
XX
DE Apurinic/apurimidinic endonuclease amino acid sequence.
XX
XX Apurinic/apurimidinic endonuclease; APE; Identification; premalignancy;
KM APE level; diagnosis; therapy; tumour; apoptosis.
XX
XX Homo sapiens.
XX
XX WO9747971-A1.
XX
XX 18-DEC-1997.
XX
XX 11-JUN-1997; 97WO-US10078.
XX
XX 11-JUN-1996; 96US-0019602.
XX
XX 11-JUN-1996; 96US-0019561.
XX
XX (ADRE-) ADVANCED RES & TECHNOLOGY INST.
XX
XX Duguid JR, Ebler JN, Kelley MR;
XX
XX WPI: 1998-168751/15.
XX
XX N-PSDB: AAV21204.
XX
XX Use of apurinic/apurimidinic endonuclease - for developing products
PT for the diagnosis and therapy of tumours, or for detecting, inducing
PT or inhibiting apoptosis in cells
XX
XX Disclosure; Pages 131-132; 166pp; English.
XX
XX The present sequence represents an apurinic/apurimidinic endonuclease
CC (APE). Levels of APE in dysplasia, carcinoma in situ and squamous cell
CC carcinomas of the cervix and prostate are substantially elevated,
CC relative to controls. A method for identifying a premalignant or
CC malignant condition in a human subject comprises determining the
CC level of APE in cells from the subject, where an elevated level of
CC APE, as compared to the APE level in corresponding normal cells,
CC indicates a premalignant or malignant condition. APE levels can be
CC used in the diagnosis and therapy of tumours. They can also be used
CC for detecting, inducing or inhibiting apoptosis in cells, e.g. for
CC treating T-cells infected with HIV or detecting apoptosis in cells
CC that have been subjected to chemo-, radio- or gene therapy.
XX
XX Sequence 318 AA;
XX
Query Match 100.0%; Score 78; DB 19; Length 318;
Best Local Similarity 100.0%; Pred. No. 0.00026;

Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEDPPD 14
DB 37 AAGEGPALEDPPD 50

RESULT 6

AAB56610
ID AAB56610 standard; Protein; 345 AA.

AC AAB56610;

DE 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SPQ ID NO:1188.

KW Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
KW neuroprotective; cytosolic; cardiostatic; immunomodulatory; muscular;
KW vulnary; gastrointestinal; nephrotoxic; anti-infective; gynaecological;
KW antibacterial; gene therapy; neural; immune; reproductive; renal;
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
KW wound; infectious disease.

OS Homo sapiens.

PN W020005174-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000MO-US05988.

PR 12-MAR-1999; 9905-0124270.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

DR WPI; 2000-587513/55.

DR N-PSDB; AAF15813.

PT Prostate cancer associated gene sequences, referred to as prostate
PT cancer antigens, useful for treatment, prevention, and diagnosis of
PT disorders such as prostate cancer -

PS Claim 11; Page 1600; 2338pp; English.

CC AAF15566 to AAF15505 encode the human prostate cancer associated
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
CC The prostate cancer antigens can have neuroprotective, cytosolic,
CC cardiostatic, immunomodulatory, muscular, vulnary, gastrointestinal,
CC nephrotoxic, anti-infective, gynaecological and antibacterial activities,
CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF15506 to AAF15514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention.

SQ Sequence 345 AA;

Query Match 100.0%; Score 78; DB 21; Length 345;

Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEDPPD 14
DB 64 AAGEGPALEDPPD 77

RESULT 7
AAW48893
ID AAW48893 standard; Protein; 524 AA.

AC AAW48893;

DE 13-OCT-1998 (first entry)

DE Homo sapiens MGMT-APE fusion protein.

KW MGMT; APE; DNA repair protein; fusion protein; AP endonuclease;
KW 0-6-methylguanine-DNA methyltransferase.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Protein 1..207

FT Protein /note="MGMT"

FT Protein 208..524

FT Protein /note="APE"

PN W09817684-A2.

PD 30-APR-1998.

PF 24-OCT-1997; 97MO-US19629.

PR 25-OCT-1996; 9605-0029308.

PA (ADRE-) ADVANCED RES & TECHNOLOGY INST.

PI Kelley M, Williams D;

DR WPI: 1998-271785/24.

DR N-PSDB; AAW32540.

PS Claim 11; p108-110; 150pp; English.

CC The sequence is that of fusion protein of the DNA repair
CC proteins 0-6-methylguanine-DNA methyltransferase (MGMT) and AP
CC endonuclease (APE). It can be used for protecting cells
CC (especially bone marrow cells) against DNA damaging agents such as
CC chemotherapeutic agents used in tumour therapy and can be used in
CC conjunction with chemotherapy to facilitate the use of increased doses
CC of chemotherapy. They can provide added protection to cells by
CC providing RPs which recognise different types of DNA lesions. In
CC addition, the FPs can be used in the treatment of DNA-repair-defective
CC human diseases, e.g. Xeroderma Pigmentosum, Ataxia Telangiectasia,
CC Cockayne's syndrome, Bloom's syndrome, Fanconi's anaemia, Parkinson's
CC disease and other neurodegenerative diseases including amyotrophic
CC lateral sclerosis, Alzheimer's disease and other age related disorders.

SQ Sequence 524 AA;

Query Match 100.0%; Score 78; DB 19; Length 524;

Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGPALEDPPD 14
DB 243 AAGEGPALEDPPD 256

RESULT 8

AAU54366
ID AAU54366 standard; Protein; 364 AA.

AC AAU54366;

```

XX 27-FEB-2002 (first entry)
XX
XX Proplionbacterium acnes immunogenic protein #15262.
DE
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hyperostosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
OS
XX Propionbacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US12865.
XX
XX 21-APR-2000; 2000US-199047P.
XX 02-JUN-2000; 2000US-208841P.
XX 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI: 2001-616774/71.
XX N-PSDB: AAS59564.
XX
XX Proplionbacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Example 1: SEQ ID No 15561; 1069pp; English.
XX
XX Sequences AAU9105-AAU68017 represent Propionbacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_ptc_sequences.
XX
XX Sequence 364 AA:
SQ

```

Query Match 57.7%; Score 45; DB 22; Length 364;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

OY 3 GEGPALYEDPPD 14
   1 1 1 1 1 1 1
Db 200 GESPVTGEDPPD 211

```

RESULT 9
AAB54099
ID AAB54099 standard; Protein; 68 AA.
XX AAB54099;

```

XX 09-MAR-2001 (first entry)
XX
XX Human pancreatic cancer antigen protein sequence SEQ ID NO:551.
DE
XX
XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
KW detection; diagnosis; identification; cytostatic; neuroprotective;
KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic;
KW neural; immune system; muscular; reproductive; gastrointestinal;
KW pulmonary; cardiovascular; renal; proliferative.
XX
XX Homo sapiens.
XX
XX WO200055320-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05989.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM;
XX WPI: 2000-579444/54.
XX N-PSDB: AAC98864.
XX
XX New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition -
XX
XX Claim 11: Page 989; 1379pp; English.
XX
XX AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention.
XX
XX Sequence 68 AA:
SQ

```

Query Match 56.4%; Score 44; DB 21; Length 68;
Best Local Similarity 61.5%; Pred. No. 12;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

OY 1 AAGEGPALYEDPP 13
   1 1 1 1 1 1 1
Db 39 AAGQEPXCLEDPP 51

```

RESULT 10
AAU47601
ID AAU47601 standard; Protein; 241 AA.
XX AAU47601;

XX AC AA047601;
XX DT 27-FEB-2002 (first entry)
XX DE Propionibacterium acnes immunogenic protein #8497.
XX KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX KW dermatological; osteopathic; neuroprotectant.
XX OS Propionibacterium acnes.
XX PN W0200181581-A2.
XX PD 01-NOV-2001.
XX PF 20-APR-2001; 2001WO-US12865.
XX PR 21-APR-2000; 2000US-199047P.
XX PR 02-JUN-2000; 2000US-208841P.
XX PR 07-JUL-2000; 2000US-216747P.
XX PA (CORI-) CORIXA CORP.
XX PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX DR WPI; 2001-616774/71.
XX DR N-PSDB; AAS59539.
XX PT Propionibacterium acnes polypeptides and nucleic acids useful for
XX PT vaccinating against and diagnosing infections, especially useful for
XX PT treating acne vulgaris -
XX PS Example 1; SEQ ID No 8796; 10699p; English.
XX PS Sequences AAU9105-AAU68017 represent Propionibacterium acnes immunogenic
XX CC polypeptides. The proteins and their associated DNA sequences are used in
XX CC the treatment, prevention and diagnosis of medical conditions caused by
XX CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX CC P. acnes is also involved in infections of bone, joints and the central
XX CC nervous system, however it is particularly involved in the inflammatory
XX CC lesions associated with acne vulgaris. A method for detecting the
XX CC presence or absence of P. acnes in a patient comprises contacting a
XX CC sample with a binding agent that binds to the proteins of the invention
XX CC and determining the amount of bound protein in the sample. The
XX CC polypeptides may be used as antigens in the production of antibodies
XX CC specific for P. acnes proteins. These antibodies can be used to
XX CC downregulate expression and activity of P. acnes polypeptides and
XX CC therefore treat P. acnes infections. The antibodies may also be used as
XX CC diagnostic agents for determining P. acnes presence. For example, by
XX CC enzyme linked immunosorbent assay (ELISA).
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 241 AA;
XX
XX Query Match 55.1%; Score 43; DB 22; Length 241;
XX Best local Similarity 80.0%; Pred. No. 62;
XX Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Oy 3 GEGPALYEDP 12
XX | | | | |
XX Db 104 GEGPALYEDP 113
XX
XX RESULT 11
XX AAG53685
XX ID AAG53685 standard; Protein; 999 AA.

XX AC AAG53685;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 68372.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0133180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
XX PR 06-APR-1999; 99US-0128234.
XX PR 08-APR-1999; 99US-0128714.
XX PR 16-APR-1999; 99US-0129845.
XX PR 19-APR-1999; 99US-0130077.
XX PR 21-APR-1999; 99US-0130449.
XX PR 23-APR-1999; 99US-0130510.
XX PR 23-APR-1999; 99US-0130891.
XX PR 28-APR-1999; 99US-0131449.
XX PR 30-APR-1999; 99US-0132048.
XX PR 30-APR-1999; 99US-0132407.
XX PR 04-MAY-1999; 99US-0132484.
XX PR 05-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 07-MAY-1999; 99US-0132487.
XX PR 11-MAY-1999; 99US-0134256.
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AC AAG53684;

XX 18-OCT-2000 (first entry)

DE Arelidopsis thaliana protein fragment SEQ ID NO: 68371.

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KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS *Arabidopsis thaliana*.
XX EPI033405-A2.
PD 06-SEP-2000.
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AC AAG53683;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68370.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

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PR 13-AUG-1999: 99US-0148684.
PR 16-AUG-1999: 99US-0149368.
PR 17-AUG-1999: 99US-0149175.
PR 18-AUG-1999: 99US-0149426.
PR 20-AUG-1999: 99US-0149722.
PR 20-AUG-1999: 99US-0149723.
PR 20-AUG-1999: 99US-0149929.
PR 23-AUG-1999: 99US-0149902.
PR 23-AUG-1999: 99US-0149930.
PR 25-AUG-1999: 99US-0150566.
PR 26-AUG-1999: 99US-0150884.
PR 27-AUG-1999: 99US-0151065.
PR 27-AUG-1999: 99US-0151066.
PR 27-AUG-1999: 99US-0151080.
PR 27-AUG-1999: 99US-0151080.
PR 30-AUG-1999: 99US-0151303.
PR 31-AUG-1999: 99US-0151308.
PR 01-SEP-1999: 99US-0151930.
PR 07-SEP-1999: 99US-0152363.
PR 10-SEP-1999: 99US-0153070.
PR 13-SEP-1999: 99US-0153758.
PR 15-SEP-1999: 99US-0154018.
PR 16-SEP-1999: 99US-0154039.
PR 20-SEP-1999: 99US-0154779.

PR 22-SEP-1999: 99US-0155139.
PR 23-SEP-1999: 99US-0155486.
PR 24-SEP-1999: 99US-0155659.
PR 28-SEP-1999: 99US-0156458.
PR 29-SEP-1999: 99US-0156596.
PR 04-OCT-1999: 99US-0157117.
PR 05-OCT-1999: 99US-0157753.
PR 06-OCT-1999: 99US-0157865.
PR 07-OCT-1999: 99US-0158029.
PR 08-OCT-1999: 99US-0158232.
PR 12-OCT-1999: 99US-0158369.
PR 13-OCT-1999: 99US-0159293.
PR 13-OCT-1999: 99US-0159294.
PR 13-OCT-1999: 99US-0159295.
PR 14-OCT-1999: 99US-0159329.
PR 14-OCT-1999: 99US-0159330.
PR 14-OCT-1999: 99US-0159331.
PR 14-OCT-1999: 99US-0159637.
PR 14-OCT-1999: 99US-0159638.
PR 18-OCT-1999: 99US-0159584.
PR 21-OCT-1999: 99US-0160741.
PR 21-OCT-1999: 99US-0160767.
PR 21-OCT-1999: 99US-0160768.
PR 21-OCT-1999: 99US-0160770.
PR 21-OCT-1999: 99US-0160814.
PR 21-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160815.
PR 22-OCT-1999: 99US-0160981.
PR 22-OCT-1999: 99US-0160989.
PR 25-OCT-1999: 99US-0161404.
PR 25-OCT-1999: 99US-0161405.
PR 25-OCT-1999: 99US-0161406.
PR 26-OCT-1999: 99US-0161359.
PR 26-OCT-1999: 99US-0161360.
PR 26-OCT-1999: 99US-0161361.
PR 28-OCT-1999: 99US-0161920.
PR 28-OCT-1999: 99US-0161992.
PR 28-OCT-1999: 99US-0161993.
PR 29-OCT-1999: 99US-0162142.

Query Match 55.1%; Score 43; DB 21; Length 1065;
Best Local Similarity 58.3%; Pred. No. 2.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 GEGPALYEDPD 14
DB 422 GEGPSLHQLPPD 433

RESULT 14
ID AAY21361 standard; protein; 115 AA.
XX AAY21361;

DT 22-JUL-1999 (first entry)
XX

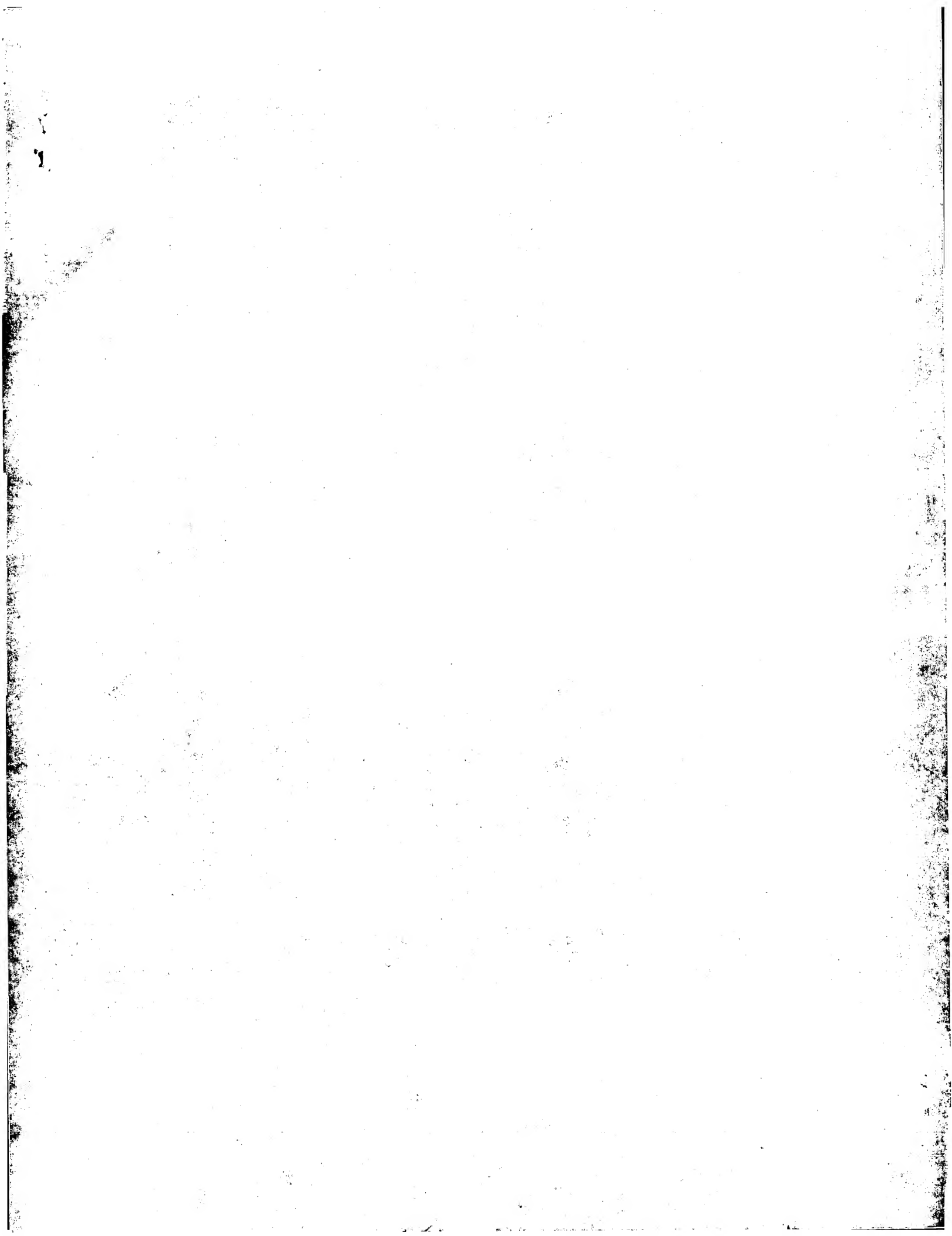
DE Human HUPF-I mutant protein fragment 13.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-I;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
XX high mobility group protein-C; neuroendocrine specific protein A.

OS Synthetic.
OS Homo sapiens.
XX

PN WO9845322-A2.
 XX
 PD 15-OCt-1998.
 XX
 PF 02-APR-1998; 98WO-1B00705.
 XX
 PR 10-APR-1997; 97US-0043163.
 XX
 PA (UYUT-) RIJKSUNIV UTRECHT.
 PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Burbach JPH, Grosveld FG, Van Leeuwen FW;
 XX
 DR WPI: 1998-609901/51.
 DR N-PSDB; AAX75768.
 XX
 PT Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also
 PT for treatment and prevention with specific ribozymes or wild-type
 PT RNA
 XX
 PS Disclosure; Figure 17; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGp-C) and neuroendocrine specific protein A.
 CC
 XX
 SQ Sequence 115 AA;
 Query Match 53.8%; Score 42; DB 19; Length 115;
 Best Local Similarity 80.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 5 GPALYEDPPD 14
 III IIIII
 Db 94 GRANGEDPPD 103
 RESULT 15
 ABB97554
 ID ABB97554 standard; Protein: 383 AA.
 XX
 AC ABB97554;
 XX
 DT 27-JUN-2002 (first entry)
 XX
 DE Novel human protein SEQ ID NO: 822.
 XX
 KW Human; antiinflammatory; antiinflammatory; immunomodulator;
 KW antifertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
 KW neuroprotective; antiparkinsonian; protein therapy; EST;
 KW expressed sequence tag.
 XX
 OS Homo sapiens.
 XX
 PN WO200222660-A2.

XX
 PD 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US26015.
 XX
 PR 11-SEP-2000; 2000US-0659671.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI: 2002-292408/33.
 DR N-PSDB; ABN32740.
 XX
 PT An isolated polynucleotide for treating diseases associated with its
 PT encoded polypeptide such as cancer and multiple sclerosis -
 XX
 PS Claim 20; SEQ ID NO 822; 509pp; English.
 XX
 CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC hematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions
 CC e.g. Rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a protein of the invention.
 XX
 SQ Sequence 383 AA;
 Query Match 53.8%; Score 42; DB 23; Length 383;
 Best Local Similarity 58.3%; Pred. No. 1.4e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 OY 1 AAGEGPALYEDP 12
 :IIIIII:II
 Db 164 SAGEGPVIVVHP 175
 Search completed: January 30, 2003, 14:37:38
 Job time : 37 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 14:35:08 ; Search time 28 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-10-001-426-2
Perfect score: 78
Sequence: 1 AAGEGSPALYEDPPD 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	96.2	69	6 097870	097870 ateles belz
2	74	94.9	289	11 099Pc3	099Pc3 rattus norv
3	64	82.1	317	11 092232	092232 cricetus
4	45	57.7	121	12 072205	072205 hepatitis c
5	45	57.7	121	12 072206	072206 hepatitis c
6	45	57.7	121	12 072207	072207 hepatitis c
7	45	57.7	121	12 072208	072208 hepatitis c
8	45	57.7	121	12 072209	072209 hepatitis c
9	45	57.7	121	12 072210	072210 hepatitis c
10	45	57.7	121	12 072211	072211 hepatitis c
11	45	57.7	186	12 091Xx0	091Xx0 hepatitis c
12	45	57.7	186	12 091Xw6	091Xw6 hepatitis c
13	45	57.7	186	12 091Xw3	091Xw3 hepatitis c
14	45	57.7	186	12 091Xw2	091Xw2 hepatitis c
15	45	57.7	186	12 091Xw1	091Xw1 hepatitis c
16	45	57.7	186	12 091Xv9	091Xv9 hepatitis c

17	45	57.7	186	12 091Xv8	091Xv8 hepatitis c
18	45	57.7	186	12 091Xv4	091Xv4 hepatitis c
19	45	57.7	438	2 054823	054823 streptomyce
20	44	56.4	328	16 08YC05	08YC05 brucella me
21	43.5	55.8	612	16 09X0L0	09X0L0 thermotoga
22	43	55.1	121	12 09W682	09W682 hepatitis c
23	43	55.1	121	12 09W685	09W685 hepatitis c
24	43	55.1	121	12 09W687	09W687 hepatitis c
25	43	55.1	186	12 091Xv0	091Xv0 hepatitis c
26	43	55.1	186	12 091Xv2	091Xv2 hepatitis c
27	43	55.1	186	12 091Xv1	091Xv1 hepatitis c
28	43	55.1	186	12 091Xv8	091Xv8 hepatitis c
29	43	55.1	186	12 091Xv7	091Xv7 hepatitis c
30	43	55.1	186	12 091Xv6	091Xv6 hepatitis c
31	43	55.1	186	12 091Xv5	091Xv5 hepatitis c
32	43	55.1	224	12 073450	073450 human papil
33	43	55.1	1006	10 08RX09	08RX09 arabidopsis
34	43	55.1	1157	17 08TK13	08TK13 methanosarc
35	43	55.1	3104	2 004846	004846 corynobacte
36	42.5	54.5	226	11 09DA92	09DA92 mus musculu
37	42	53.8	157	6 095Mv7	095Mv7 equus caball
38	42	53.8	186	12 091Xv7	091Xv7 hepatitis c
39	42	53.8	186	12 091Xv5	091Xv5 hepatitis c
40	42	53.8	303	4 09UBE5	09UBE5 homo sapien
41	42	53.8	331	16 0920A9	0920A9 rhizobium m
42	42	53.8	392	11 0921Z6	0921Z6 rattus norv
43	42	53.8	583	5 09YVH5	09YVH5 drosophila
44	42	53.8	945	6 09N175	09N175 ovis aries
45	42	53.8	1017	4 09H9B8	09H9B8 homo sapien

ALIGNMENTS

RESULT 1
097870 ID 097870 PRELIMINARY: PRT: 69 AA.

AC 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE APEX nuclease (Fragment).
GN APX.
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles.
OX NCBI_TaxID=118643;
RN [1]
RP SEQUENCE FROM N.A.
RA Canavez F.C., Senanez H.N.;
RT "Gene assignment in the spider monkey (Ateles paniscus chamek-APC):
RT APE-MHV7 to 2q: AR-GUA-F8C to the X chromosome.";
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF064685; AAD17542.1; -
DR HSSP: P27695; 1BIX.
DR InterPro: IPR00097; Appendicisel.
DR InterPro: IPR005135; Exo_endo_phos.
DR Pfam: PF03372; Exo_endo_phos; 1.
DR PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 69 AA: 7583 MW: 2FF30737F1581DD4 CRC64;

Query Match 96.2% Score 75; DB 6; Length 69;
Best local similarity 92.9% Pred. No. 3.1e-05;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGEGSPALYEDPPD 14
Db 1 AAGEGSPALYEDPPD 14
RESULT 2

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099PF3
ID 099PF3 PRELIMINARY; PRT; 289 AA.
AC 099PF3;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE APEX (Fragment).
GN APEX.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NORMAY;
RA Xie Z.H., Liu C.Z., He Y.H., Wang A.M., Ma C.;
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF311054; AAC49922.1; -.
DR HSSP: P27695; 1BIX.
DR InterPro: IPR000097; Appendicisel.
DR InterPro: IPR004442; ExoDNase_III.
DR InterPro: IPR004808; ExoIII_xth.
DR InterPro: IPR005135; Exo_endo_phos.
DR Pfam: PF03372; Exo_endo_phos; 1.
DR TIGRFAMS: TIGR00195; exoDNase_III; 1.
DR TIGRFAMS: TIGR00633; xth; 1.
DR PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.
DR PROSITE: PS00727; AP_NUCLEASE_F1_2; 1.
DR PROSITE: PS00728; AP_NUCLEASE_F1_3; 1.
FT NON_TER 1
SQ SEQUENCE 289 AA; 32353 MW; 67E82454D062CE51 CRC64;

Query Match 94.9%; Score 74; DB 11; Length 289;
Best Local Similarity 92.9%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
DB 31 AAGEGPALYEDPPD 44

RESULT 3
092J22
ID 092J22 PRELIMINARY; PRT; 317 AA.
AC 092J22;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Apurinic/apurimidinic endonuclease.
GN APE.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20075118; PubMed=10606812;
RA Purohit S., Arenaz P.;
RT "Molecular cloning, sequence and structure analysis of hamster
apurinic/apurimidinic endonuclease (chapel) gene.";
RL Mutat. Res. 435:215-224(1999).
DR EMBL: AF056934; AAD02702.1; -.
DR HSSP: P27695; 1E9N.
DR InterPro: IPR000097; Appendicisel.
DR InterPro: IPR004442; ExoDNase_III.
DR InterPro: IPR004808; ExoIII_xth.
DR InterPro: IPR005135; Exo_endo_phos.
DR Pfam: PF03372; Exo_endo_phos; 1.
DR TIGRFAMS: TIGR00195; exoDNase_III; 1.
DR TIGRFAMS: TIGR00633; xth; 1.
DR PROSITE: PS00726; AP_NUCLEASE_F1_1; 1.

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DR PROSITE: PS00727; AP_NUCLEASE_F1_2; 1.
DR PROSITE: PS00728; AP_NUCLEASE_F1_3; 1.
KW Endonuclease.
SQ SEQUENCE 317 AA; 35512 MW; 76DD6F3975455408 CRC64;

Query Match 82.1%; Score 64; DB 11; Length 317;
Best Local Similarity 85.7%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
DB 36 AAGEGPALYEDPAD 49

RESULT 4
072205
ID 072205 PRELIMINARY; PRT; 121 AA.
AC 072205;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANTI-D RECIPIENT 1;
RX MEDLINE=98241727; PubMed=9573256;
RA McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L.,
RT "Long-term evolution of the hypervariable region of hepatitis C virus
in a common source-infected cohort.";
RL J. Virol. 72:4893-4905(1998).
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL: AF056772; AAC17268.1; -.
DR InterPro: IPR002519; HCV_env.
DR InterPro: IPR002531; HCV_NS1.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NS1; 1.
DR ProDom: PD186062; HCV_NS1; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 121 AA; 13281 MW; 8401C2D7374EPCBD CRC64;

Query Match 57.7%; Score 45; DB 12; Length 121;
Best Local Similarity 57.1%; Pred. No. 5.9;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAGEGPALYEDPPD 14
DB 101 AOGWGPITYAEPD 114

RESULT 5
072206
ID 072206 PRELIMINARY; PRT; 121 AA.
AC 072206;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-ANTI-D RECIPIENT 1;
 RX MEDLINE-98241727; PubMed-9573256;
 RA McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L.,
 RA Simmonds P., Smith D.B.;
 RT "Long-term source-infected cohort."
 RT In a common-source-infected cohort."
 RL J. Virol. 72:4893-4905(1998).
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: AF056773; AAC17269.1; -.
 DR InterPro: IPR002519; HCV_env.
 DR InterPro: IPR002531; HCV_NSI.
 DR Pfam: PF01539; HCV_env; 1.
 DR Pfam: PF01560; HCV_NSI; 1.
 DR ProDom: PD186062; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13281 MW; 8401C2D7374FDC8D CRC64;

Query Match 57.7%; Score 45; DB 12; Length 121;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14
 | | | | | : | | | |
 Db 101 AAGMGPTTVAEPPD 114

RESULT 6
 072207 PRELIMINARY; PRT; 121 AA.

AC 072207;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
 DE (NS1)] (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ANTI-D RECIPIENT 1;
 RX MEDLINE-98241727; PubMed-9573256;
 RA McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L.,
 RA Simmonds P., Smith D.B.;
 RT "Long-term evolution of the hypervariable region of hepatitis C virus
 RT in a common-source-infected cohort."
 RL J. Virol. 72:4893-4905(1998).
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: AF056774; AAC17270.1; -.
 DR InterPro: IPR002519; HCV_env.
 DR InterPro: IPR002531; HCV_NSI.
 DR Pfam: PF01539; HCV_env; 1.
 DR Pfam: PF01560; HCV_NSI; 1.
 DR ProDom: PD186062; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13254 MW; B04523A965CA1367 CRC64;

Query Match 57.7%; Score 45; DB 12; Length 121;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14
 | | | | | : | | | |
 Db 101 AAGMGPTTVAEPPD 114

RESULT 7
 072208 PRELIMINARY; PRT; 121 AA.

AC 072208;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
 DE (NS1)] (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ANTI-D RECIPIENT 1;
 RX MEDLINE-98241727; PubMed-9573256;
 RA McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L.,
 RA Simmonds P., Smith D.B.;
 RT "Long-term evolution of the hypervariable region of hepatitis C virus
 RT in a common-source-infected cohort."
 RL J. Virol. 72:4893-4905(1998).
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: AF056775; AAC17271.1; -.
 DR InterPro: IPR002519; HCV_env.
 DR InterPro: IPR002531; HCV_NSI.
 DR Pfam: PF01539; HCV_env; 1.
 DR Pfam: PF01560; HCV_NSI; 1.
 DR ProDom: PD186062; HCV_NSI; 1.
 KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
 KW Polypeptide; Transmembrane.
 FT NON_TER 1
 FT NON_TER 121
 SQ SEQUENCE 121 AA; 13284 MW; A2C7B3A0FC5A087C CRC64;

Query Match 57.7%; Score 45; DB 12; Length 121;
 Best Local Similarity 57.1%; Pred. No. 5.9;
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AAGEGPALYEDPPD 14
 | | | | | : | | | |
 Db 101 AAGMGPTTVAEPPD 114

RESULT 8
 072209 PRELIMINARY; PRT; 121 AA.

AC 072209;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
 DE (NS1)] (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ANTI-D RECIPIENT 1;
 RX MEDLINE-98241727; PubMed-9573256;
 RA McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L.,
 RA Simmonds P., Smith D.B.;
 RT "Long-term evolution of the hypervariable region of hepatitis C virus
 RT in a common-source-infected cohort."
 RL J. Virol. 72:4893-4905(1998).
 CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
 DR EMBL: AF056776; AAC17272.1; -.
 DR InterPro: IPR002519; HCV_env.
 DR InterPro: IPR002531; HCV_NSI.
 DR Pfam: PF01539; HCV_env; 1.
 DR Pfam: PF01560; HCV_NSI; 1.
 DR ProDom: PD186062; HCV_NSI; 1.

KM	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW	Polyprotein; Transmembrane.
FT	NON_TER 1
FT	NON_TER 121
SO	SEQUENCE 121 AA; 13268 MW; A2C7B3BBE75A1367 CRC64;
 Query Match	
Best Local Similarity	57.7%; Score 45; DB 12; Length 121;
Matches	8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY	1 AAGEGPALYEPPD 14 :
Db	101 AQGMCPTTYAEPPD 114
 RESULT 9	
O72210	PRELIMINARY; PRT; 121 AA.
ID	072210
AC	072210:
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)] (Fragment).
OS	Hepatitis C virus.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
OX	NCBI_TaxID=11103;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-ANTI-D RECIPIENT 1;
RA	MEDLINE=98241727; PubMed=9573256;
RX	McAllister J., Casino C., Davidson F., Power J., Lawlor E., Yap P.L., Simmonds P., Smith D.B.;
RT	"Long-term evolution of the hypervariable region of hepatitis C virus in a common-source-infected cohort.";
RL	J. Virol. 72:4893-4905(1998).
CC	-I- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR	EMBL; AF056777; AAC1723.1; -
DR	InterPro; IPR002519; HCV_env.
DR	InterPro; IPR002531; HCV_NS1.
DR	Pfam; PF01539; HCV_env; 1.
DR	Pfam; PF01560; HCV_NS1; 1.
DR	proDom; PD186062; HCV_NS1; 1.
KW	Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW	Polyprotein; Transmembrane.
FT	NON_TER 1
FT	NON_TER 121
SO	SEQUENCE 121 AA; 13268 MW; A2C7B3BBE75A1367 CRC64;
 Query Match	
Best Local Similarity	57.7%; Score 45; DB 12; Length 121;
Matches	8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
OY	1 AAGEGPALYEPPD 14 :
Db	101 AQGMCPTTYAEPPD 114
 RESULT 10	
O72211	PRELIMINARY; PRT; 121 AA.
ID	072211
AC	072211:
DT	01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	Genome polyprotein [Contains: envelope glycoprotein E2 (GP68) (GP70) (NS1)] (Fragment).
OS	Hepatitis C virus.
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
OX	NCBI_TaxID=11103;
RN	[1]

QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
QY	DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74																										


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RESULT 12
O91XW6 PRELIMINARY: PRT: 186 AA.
AC O91XW6;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P10;
RX Farci P., Shlimoda A., Colana A., Diaz G., Peddis G., Melpolder J.C.,
RA Strazzer A., Chien D.Y., Munoz S.J., Balestrieri A., Purcell R.H.,
RA Alter H.J.;
RT "The outcome of acute hepatitis C predicted by the evolution of the
RT viral quasispecies."
RL Science 288:339-344(2000).
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL: AF246082; AAF66381.1; -.
DR InterPro: IPR002519; HCV_env.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NSI; 1.
DR ProDom: PD186062; HCV_NSI; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 186
SO SEQUENCE 186 AA; 20282 MW; 783A7DFCE1B41094 CRC64;

Query Match 57.7%; Score 45; DB 12; Length 186;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AGECPALYEDPPD 14
Db 149 AOGMGPTTVAEPPD 162

RESULT 13
O91XW3 PRELIMINARY: PRT: 186 AA.
AC O91XW3;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P10;
RX MEDLINE-20230065; PubMed-10764648;
RA Farci P., Shlimoda A., Colana A., Diaz G., Peddis G., Melpolder J.C.,
RA Strazzer A., Chien D.Y., Munoz S.J., Balestrieri A., Purcell R.H.,
RA Alter H.J.;
RT "The outcome of acute hepatitis C predicted by the evolution of the
RT viral quasispecies."
RL Science 288:339-344(2000).
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL: AF246082; AAF66381.1; -.
DR InterPro: IPR002519; HCV_env.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NSI; 1.
DR ProDom: PD186062; HCV_NSI; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 186
SO SEQUENCE 186 AA; 20282 MW; 783A7DFCE1B41094 CRC64;

Query Match 57.7%; Score 45; DB 12; Length 186;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AGECPALYEDPPD 14
Db 149 AOGMGPTTVAEPPD 162

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DR InterPro: IPR002531; HCV_NSI.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NSI; 1.
DR ProDom: PD186062; HCV_NSI; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 186
SO SEQUENCE 186 AA; 20280 MW; F056A403DEDFB1C CRC64;

Query Match 57.7%; Score 45; DB 12; Length 186;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AGECPALYEDPPD 14
Db 149 AOGMGPTTVAEPPD 162

RESULT 14
O91XW2 PRELIMINARY: PRT: 186 AA.
AC O91XW2;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P10;
RX MEDLINE-20230065; PubMed-10764648;
RA Farci P., Shlimoda A., Colana A., Diaz G., Peddis G., Melpolder J.C.,
RA Strazzer A., Chien D.Y., Munoz S.J., Balestrieri A., Purcell R.H.,
RA Alter H.J.;
RT "The outcome of acute hepatitis C predicted by the evolution of the
RT viral quasispecies."
RL Science 288:339-344(2000).
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL: AF246086; AAF66385.1; -.
DR InterPro: IPR002519; HCV_env.
DR Pfam: PF01539; HCV_env; 1.
DR Pfam: PF01560; HCV_NSI; 1.
DR ProDom: PD186062; HCV_NSI; 1.
KM Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 186
SO SEQUENCE 186 AA; 20237 MW; CEC976E5527C741E CRC64;

Query Match 57.7%; Score 45; DB 12; Length 186;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 AGECPALYEDPPD 14
Db 149 AOGMGPTTVAEPPD 162

RESULT 15
O91XW1 PRELIMINARY: PRT: 186 AA.
AC O91XW1;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Genome polyprotein [contains: envelope glycoprotein E2 (GP68) (GP70)
DE (NS1)] (Fragment).

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OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-P10;
RX MEDLINE=20230065; PubMed=10764648;
RA Farci P., Shioda A., Coiana A., Diaz G., Peddis G., Melpolder J.C.,
RA Strazzer A., Chien D.Y., Munoz S.J., Balestrieri A., Purcell R.H.,
RA Alter H.J.;
RT "The outcome of acute hepatitis C predicted by the evolution of the
RT viral quasispecies.";
RT Science 288:339-344(2000).
CC -1- SIMILARITY: TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN E1.
DR EMBL; AF246087; AAF66386.1; -.
DR InterPro; IPR002519; HCV_env.
DR InterPro; IPR002531; HCV_NSL.
DR Pfam; PF01539; HCV_env; 1.
DR Pfam; PF01560; HCV_NSL; 1.
DR ProDom; PD186062; HCV_NSL; 1.
KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
KW Polyprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 186 AA; 20293 MW; BAD07F7DEF4EB197 CRC64;

Query Match 57.7%; Score 45; DB 12; Length 186;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 AAGGPGALYEDPPD 14
| | | | | : | | |
Db 149 AAGGPGITVAEPPD 162

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Search completed: January 30, 2003, 14:38:31
 Job time : 29 secs